



	MS-GPC- 8-27-7	MS-GPC- 8-27-10	MS-GPC- 8-6-13	MS-GPC- 8-27-41	MS-GPC- 8-6-47	MS-GPC- 8-10-57	MS-GPC- 8-6-27	MS-GPC- 8	MS-GPC- 8-6
Plastic	-0.004	-0.020	-0.022	-0.025	-0.001	0.005	0.007	-0.022	-0.018
BSA	-0.003	-0.019	-0.021	-0.022	0.008	0.003	0.003	-0.016	-0.019
Testosterone									
-BSA	-0.005	-0.010	-0.012	-0.007	0.011	0.003	0.002	-0.009	-0.012
Lysozyme	-0.005	-0.079	-0.079	-0.073	0.013	0.014	0.006	-0.081	-0.072
human									
Apotransferrin	-0.009	-0.016	-0.018	-0.018	-0.005	-0.008	-0.004	-0.014	-0.016
MHCII (DRA*0101/ DRB1*0401)	1.549	1.493	1.467	1.525	1.400	1.256	1.297	1.058	1.306

Fig. 1A

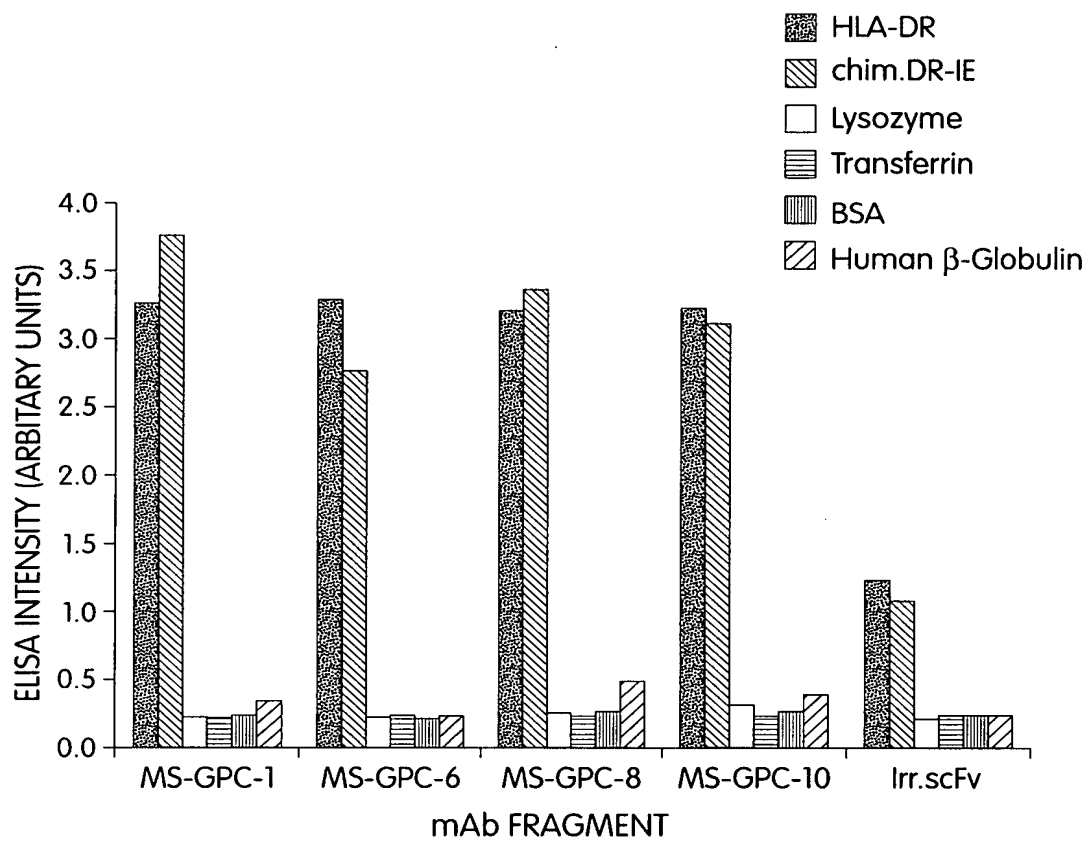


Fig. 1 B

Target Proteins	scFv												IgG		
	17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3
DR4Dw4 Purified	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chimeric DR-IE purified	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Lysozyme	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Transferrin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BSA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Human gamma globulin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

a. In Elisa, OD (at 370 nm - background): > 1.5

b. In Elisa, OD (at 370 nm - background): < 0.5

Fig. 1C

Cell Line	HLA-	DRB1*	scFv												IgG		
			17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	IC7277	305D3
LG2	DR1	0101	+	+	^b	-	+	+	+	+	+	+	+	+	+	+	+
E4181324	DR2	15021	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
VAVY	DR3	0301	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
PRIESS	DR4Dw4	0401	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+/- ^c
TS10	DR4Dw10	0402	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+
BIN40	DR4Dw14	0404	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+
TAB089	DR8	8031	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+
DKB	DR9	9012	+	+	+/-	+/-	+	+	+	+	+	+	+	+	+	+	+/-
WT47	DR13	1302	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
TEM	DR14	1401	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+
L105.1	DRw52	B3*0101	+	-	-	-	nt ^d	+	-	+	+	+	nt	nt	+/-	+/-	+/-
L257.6	DRw53	B4*0101	+/-	-	+	-	nt	+	-	+	+/-	+/-	nt	nt	+	+	+
L25.4	DPw4/w4.2	DP0103/0402	-	-	-	-	nt	+	-	-	-	-	nt	nt	+/-	-	+/-
L256.12	DPw2/w2.1	DP0202/0201	-	-	-	-	nt	+/-	-	-	-	-	nt	nt	-	-	-
L21.3	DQ7/w2	DQ0201/0602	-	-	-	-	nt	+	-	+	-	-	nt	nt	nt	nt	nt
Target Cell			% Cells Killed ^e														
PRIESS			75	20	28	32	22	89	33	59	75	34	1	5	88	93	74

a. FACS analysis, mAb + FITC-anti human IgG₄, mean fluorescence intensity > 30.

b. Mean fluorescence intensity < 10.

c. Mean fluorescence intensity 10-30.

d. Not tested.

e. Based on viable cell recovery after treatment with 200nM scFv plus 100 nM anti-FLAG or 50 nM mab at 37°C for 4h. Determined by light.

Fig. 2

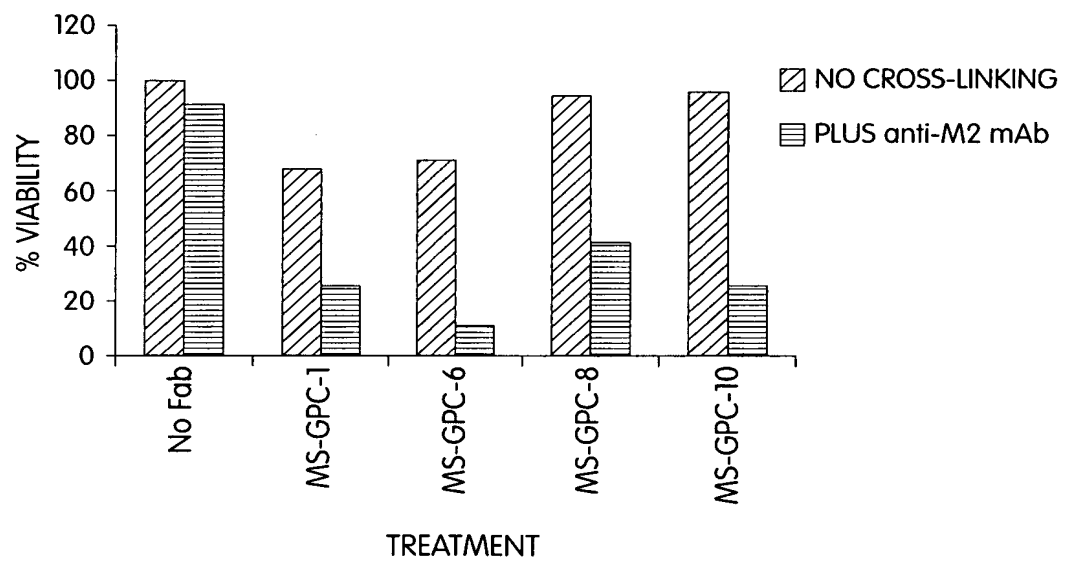


Fig. 3

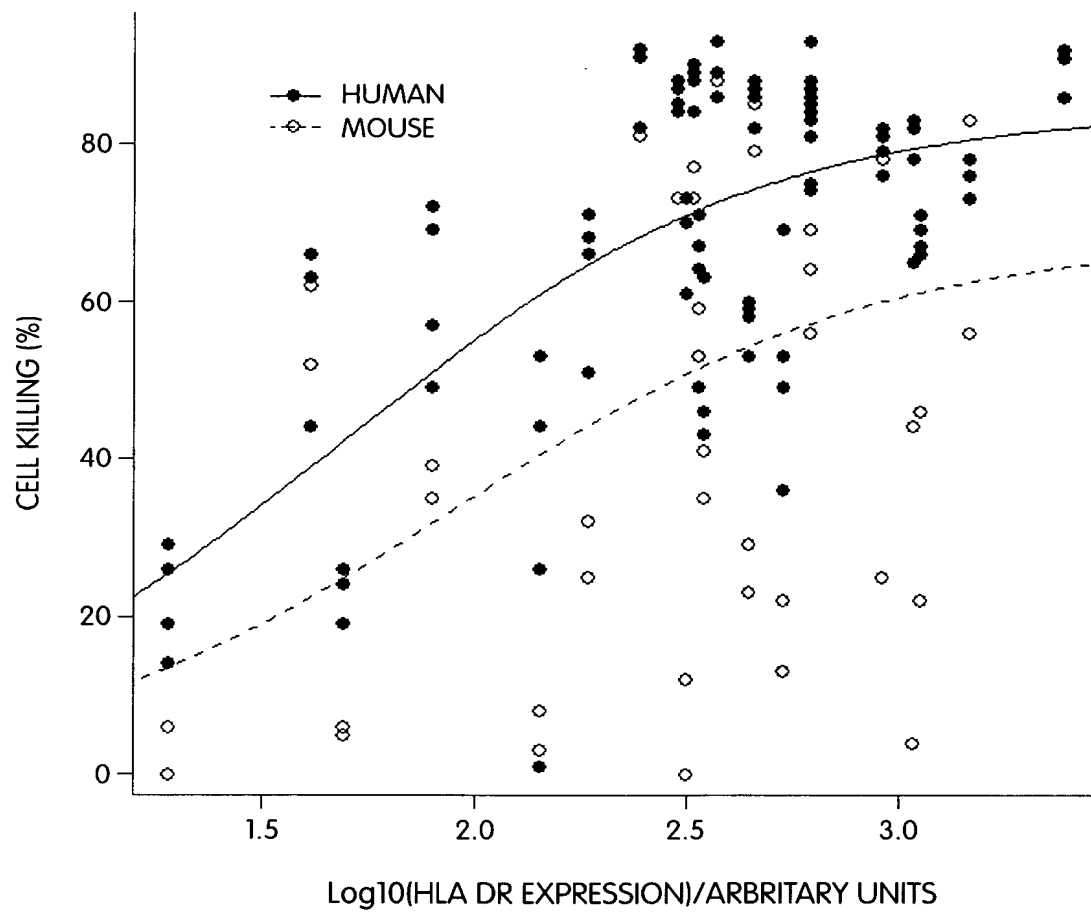


Fig. 4

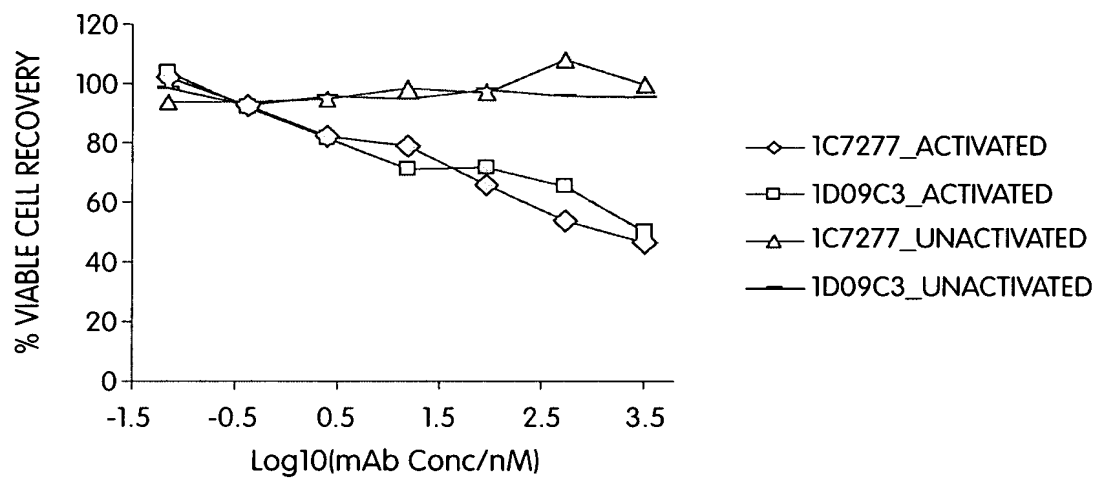


Fig. 5

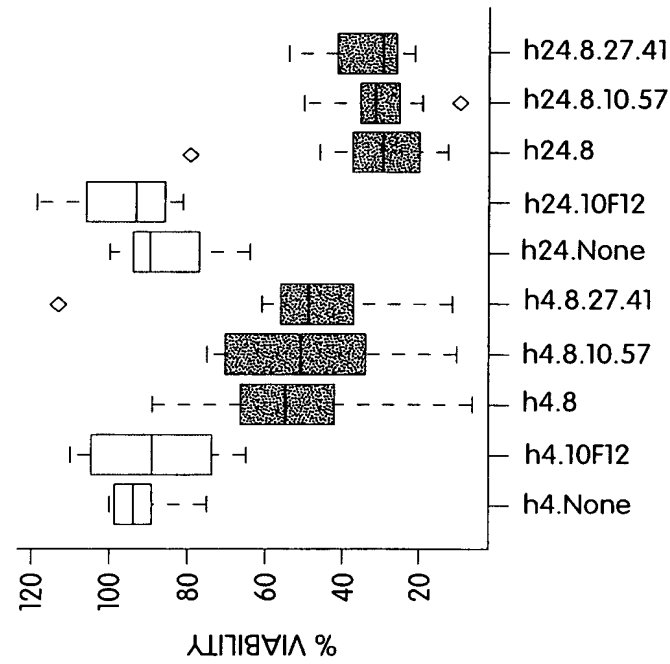
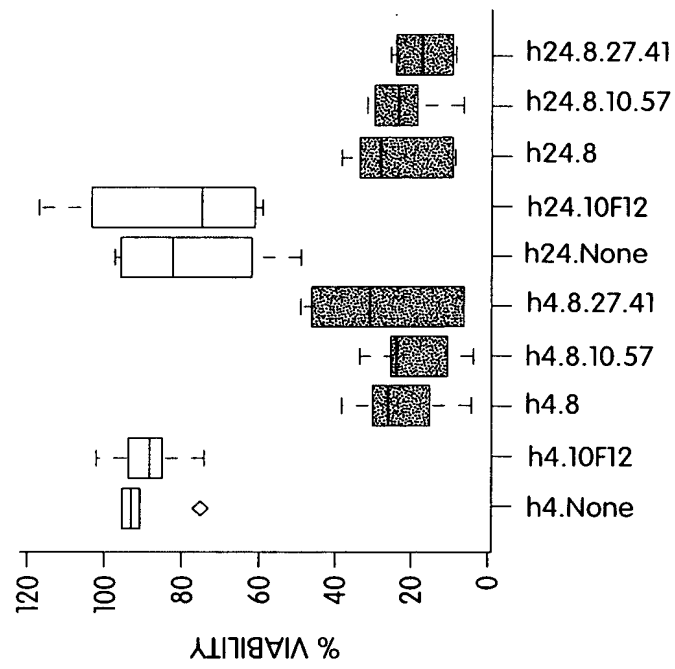
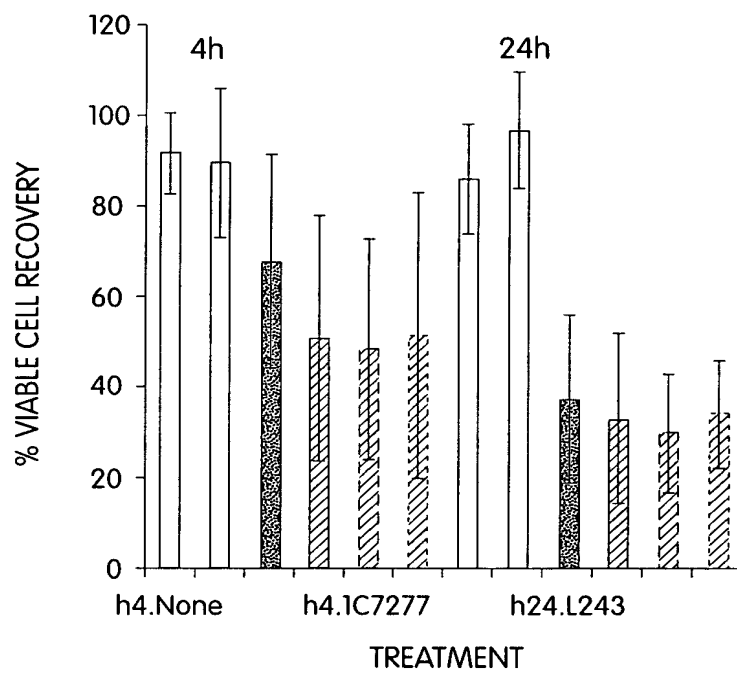


Fig. 6A

**Fig. 6B**

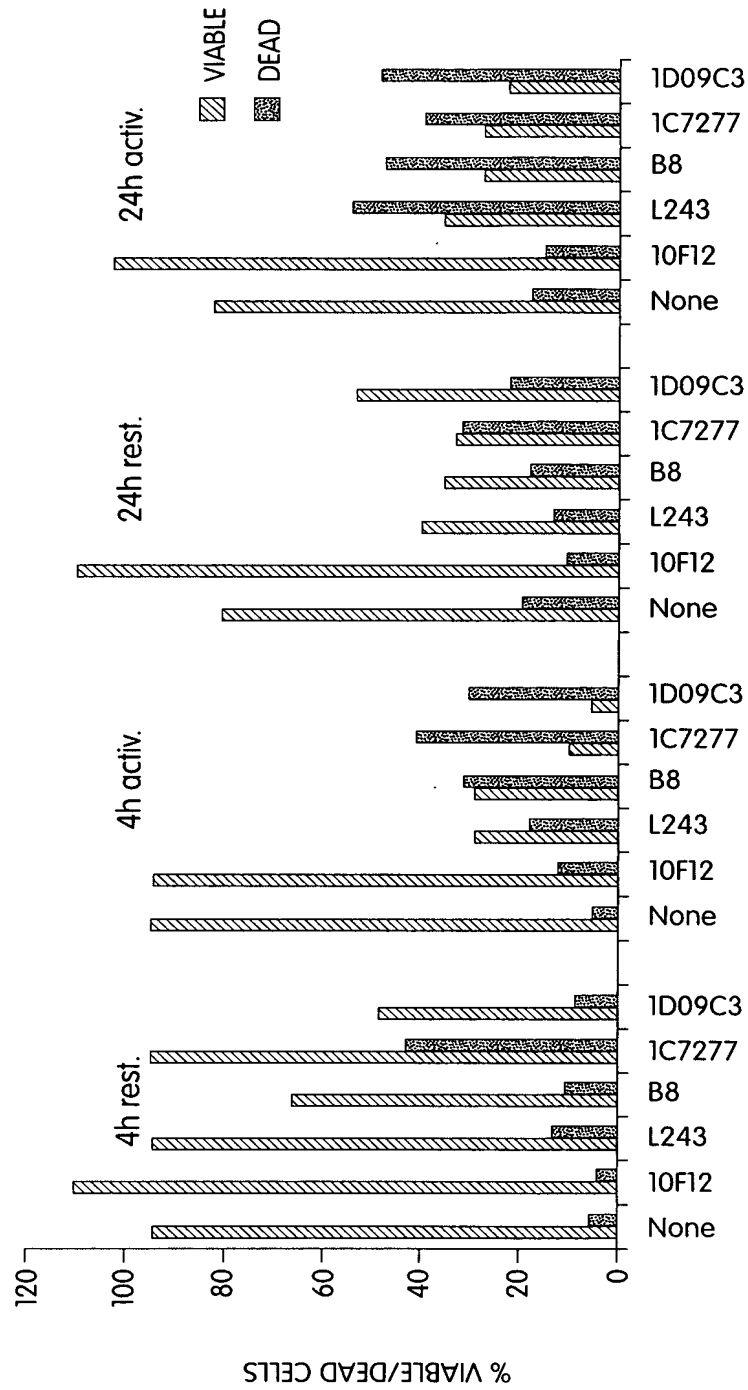


Fig. 6C

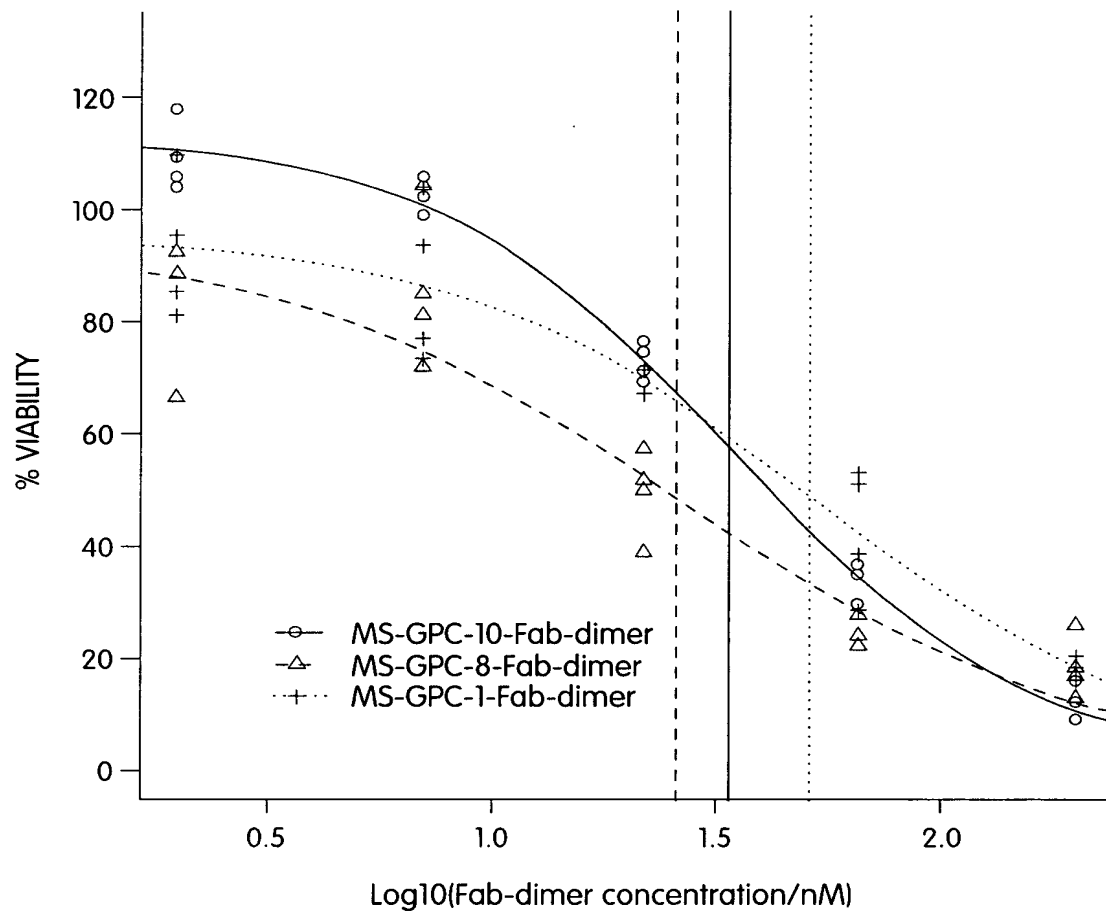


Fig. 7A

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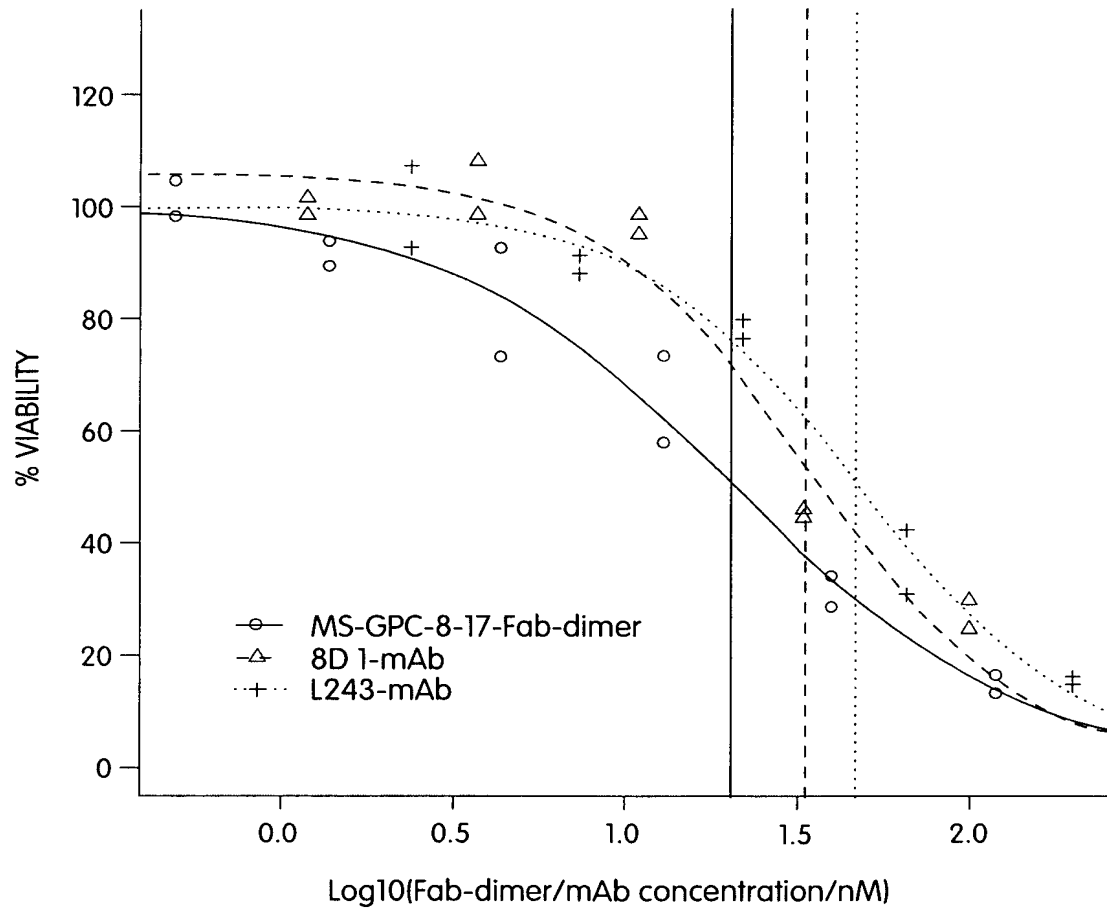


Fig. 7B

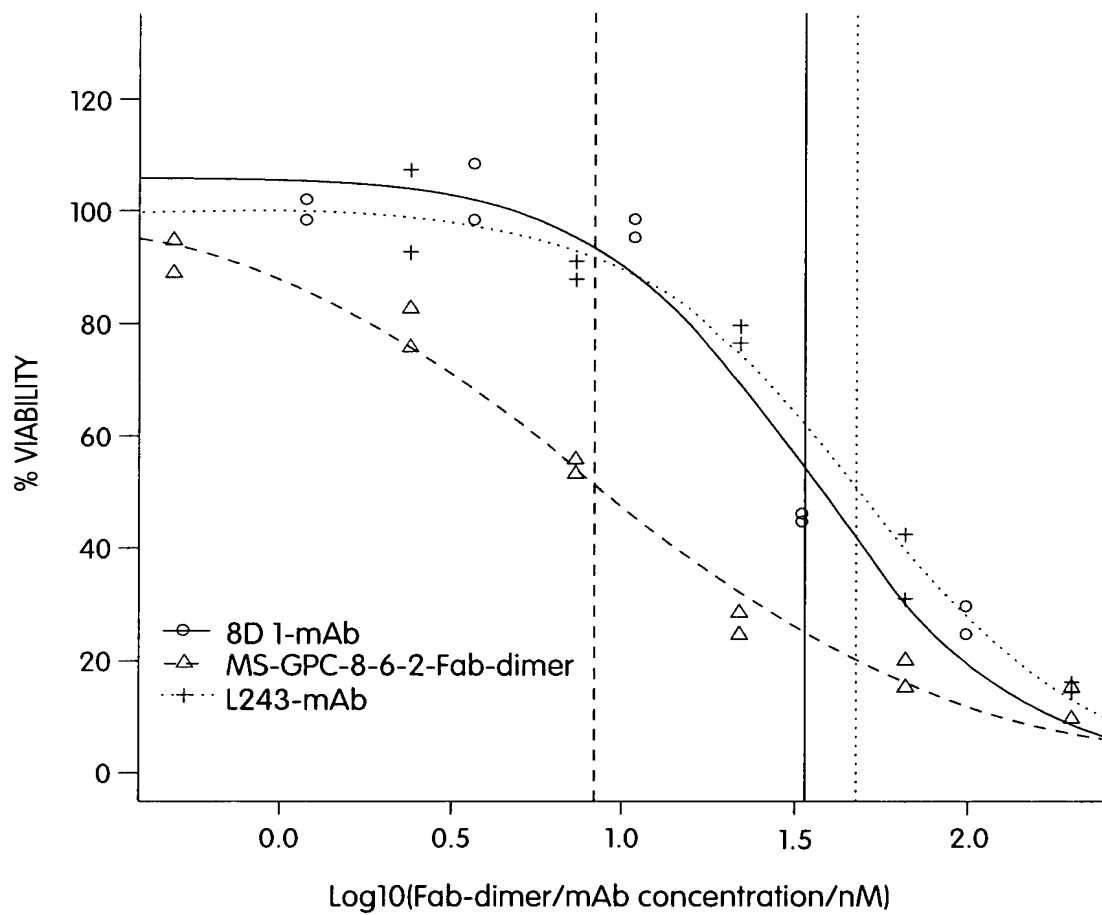


Fig. 7C

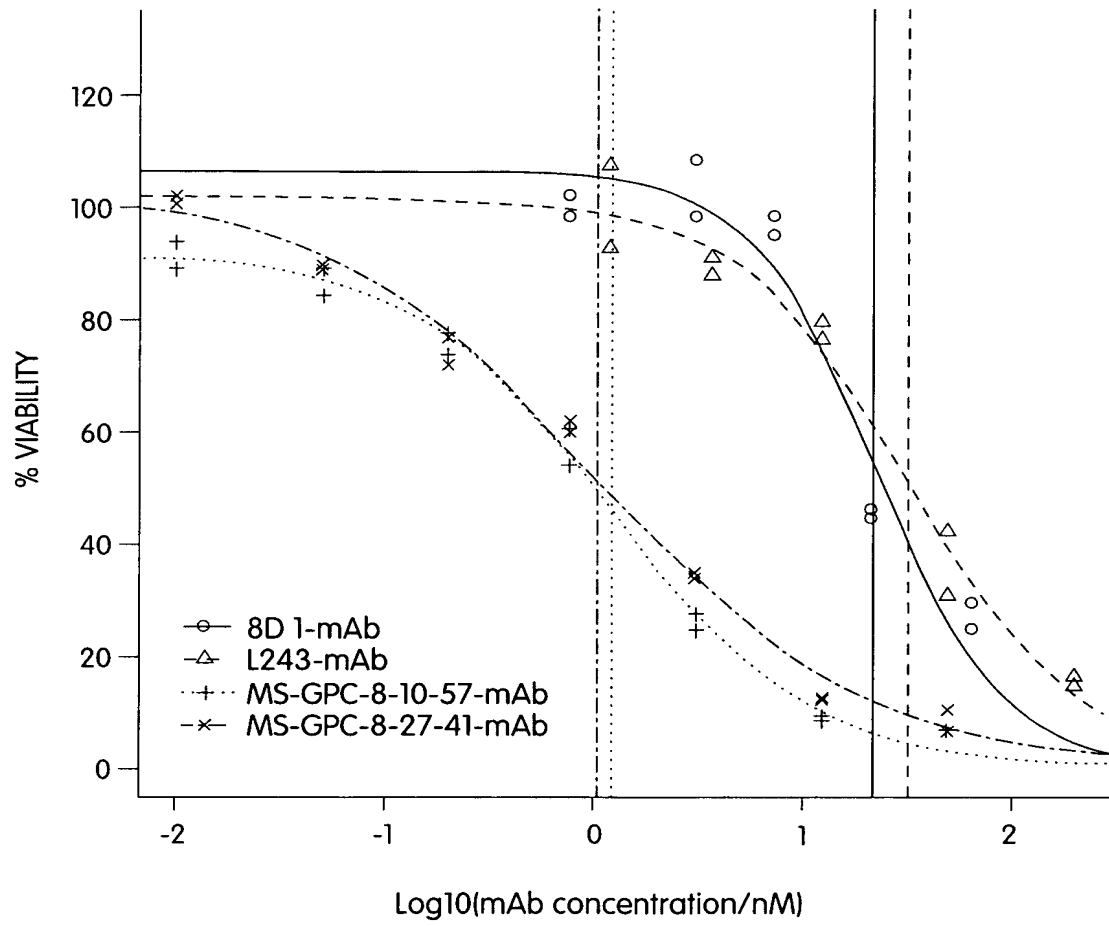


Fig. 7D

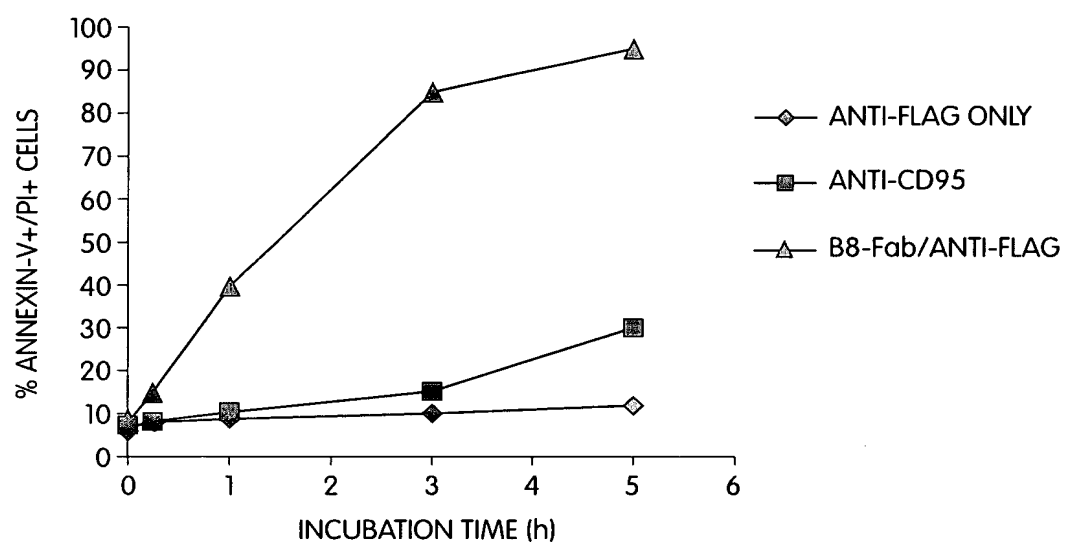


Fig. 8A

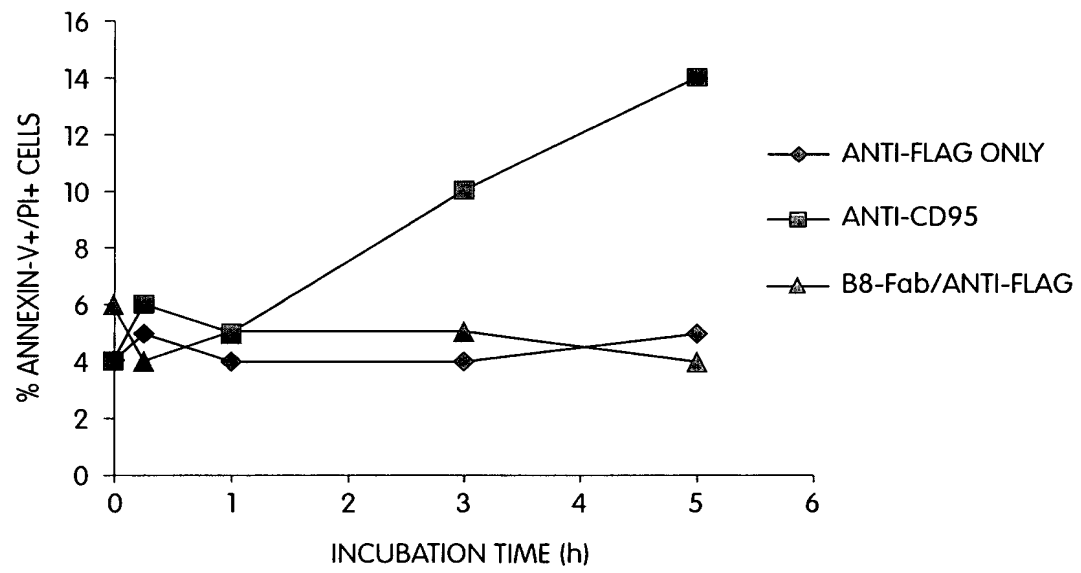


Fig. 8B

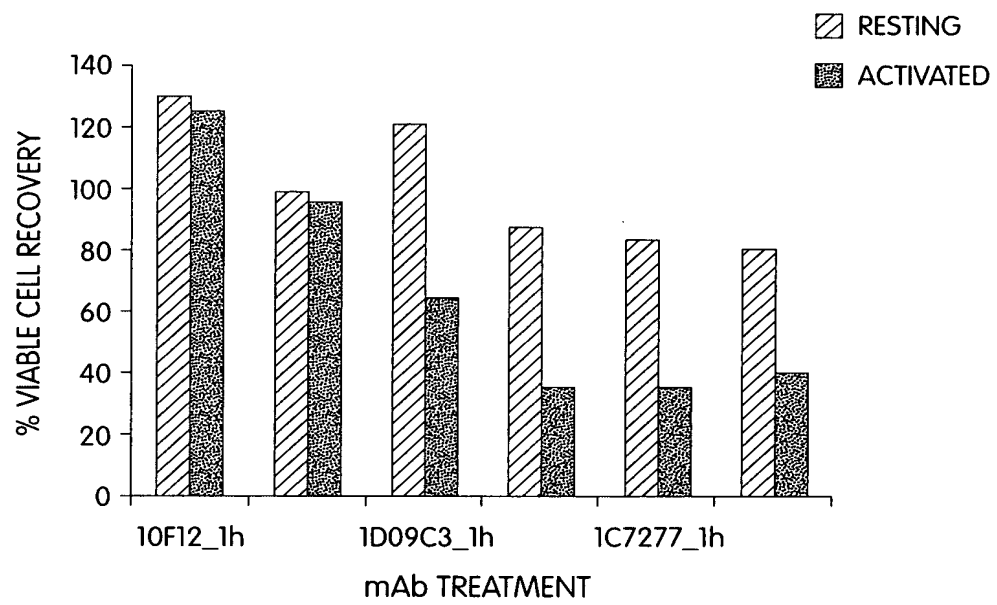


Fig. 8C

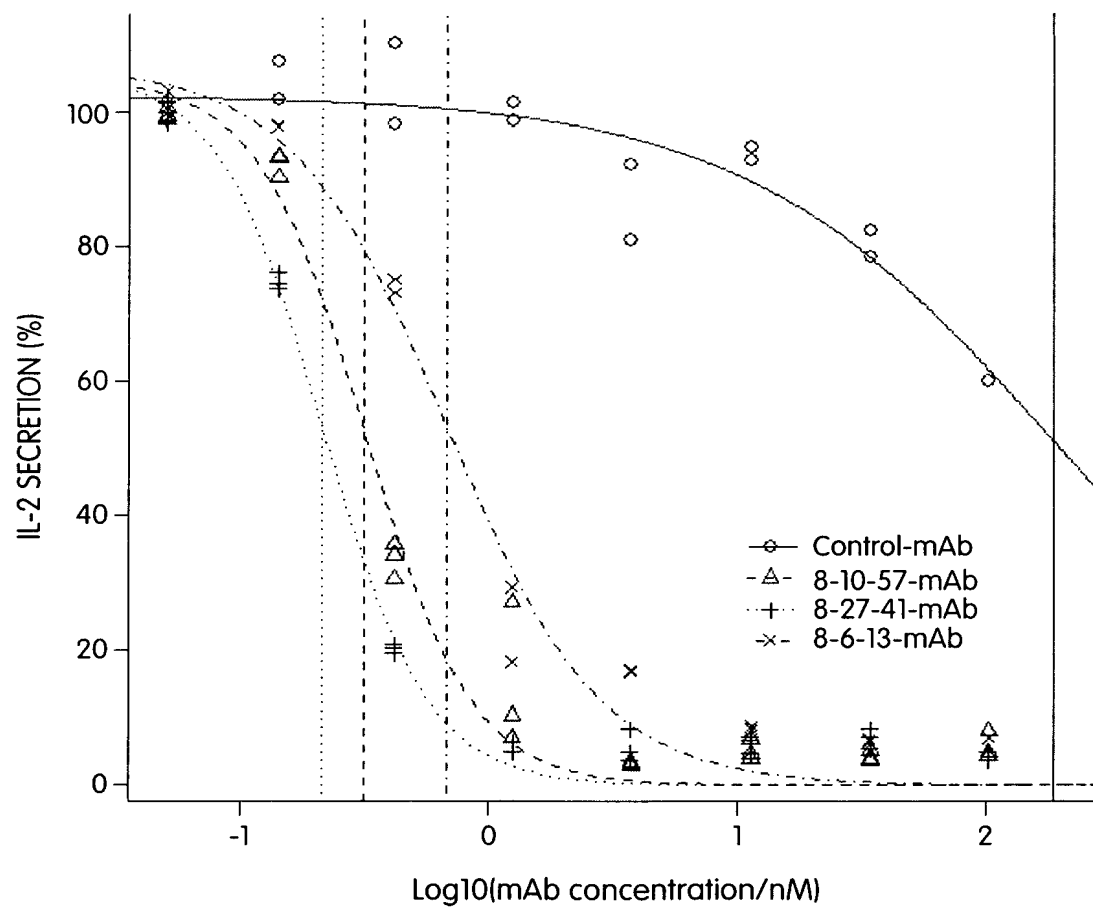


Fig. 9A

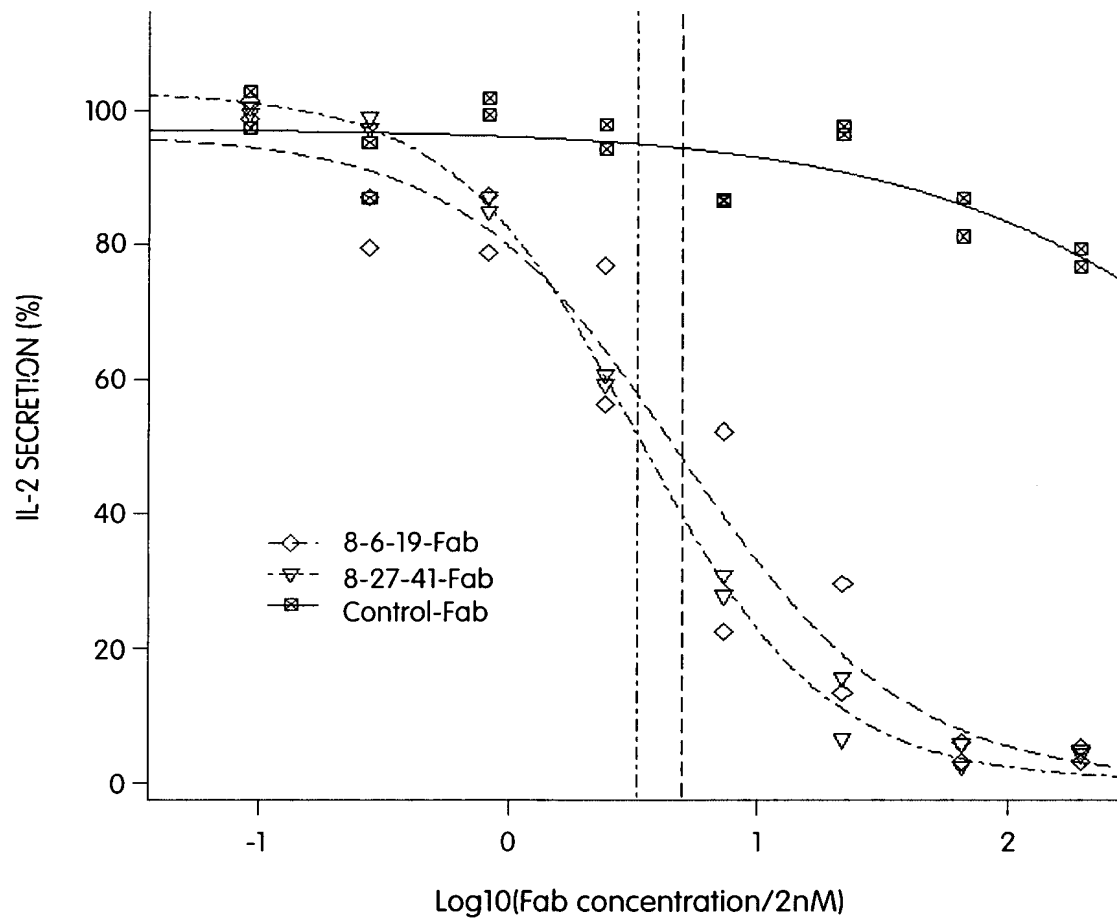


Fig. 9B

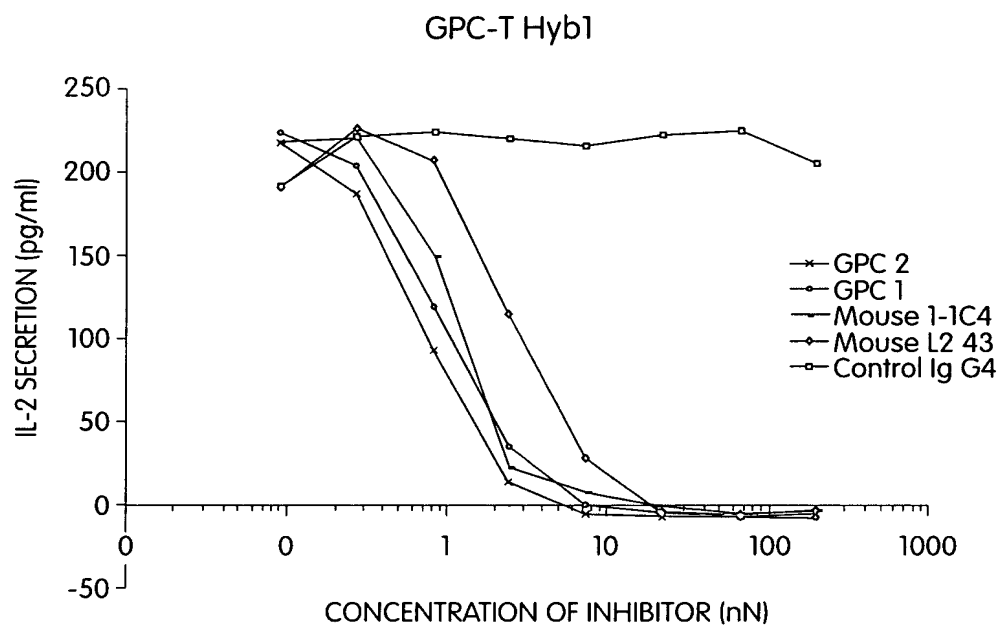


Fig. 9C

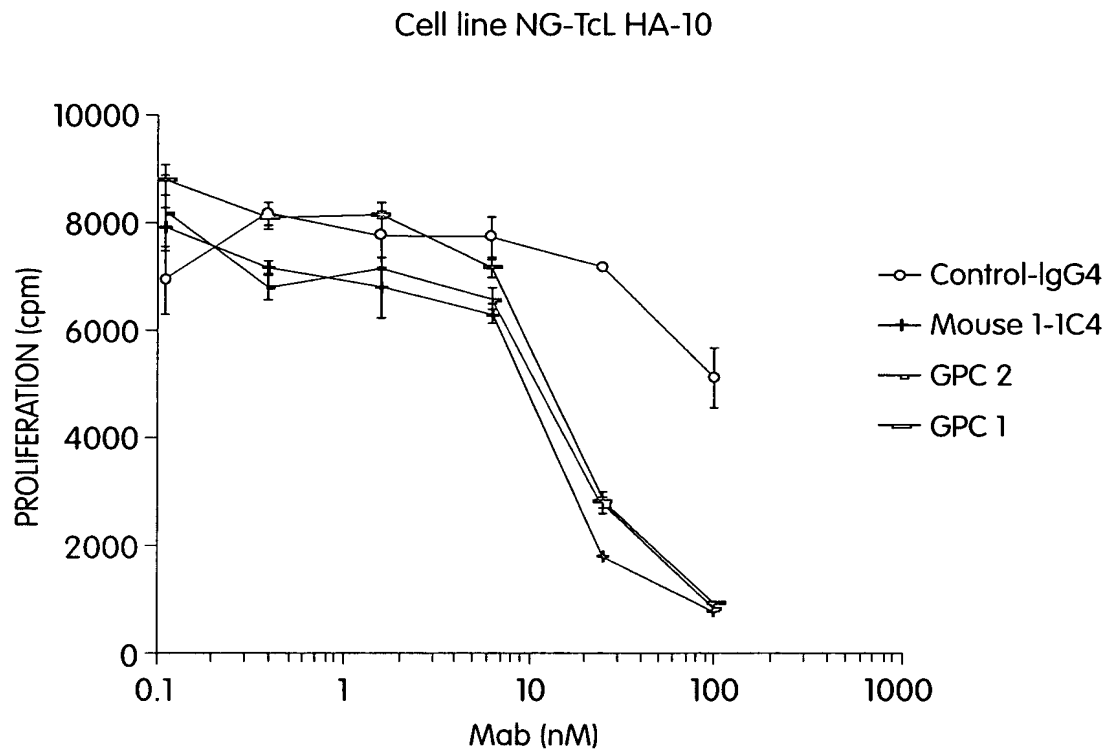


Fig. 9D

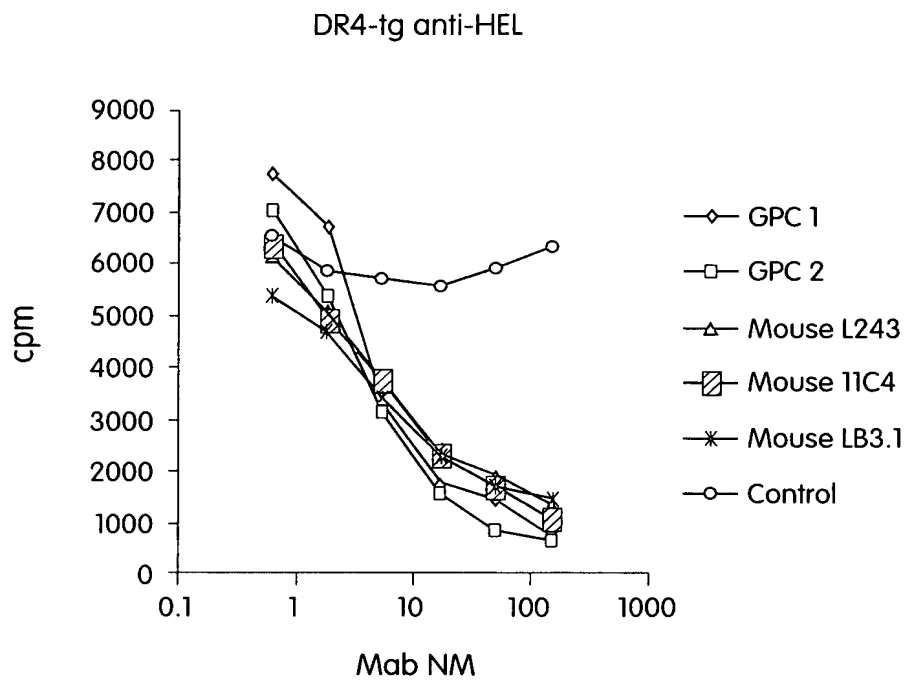


Fig. 9E

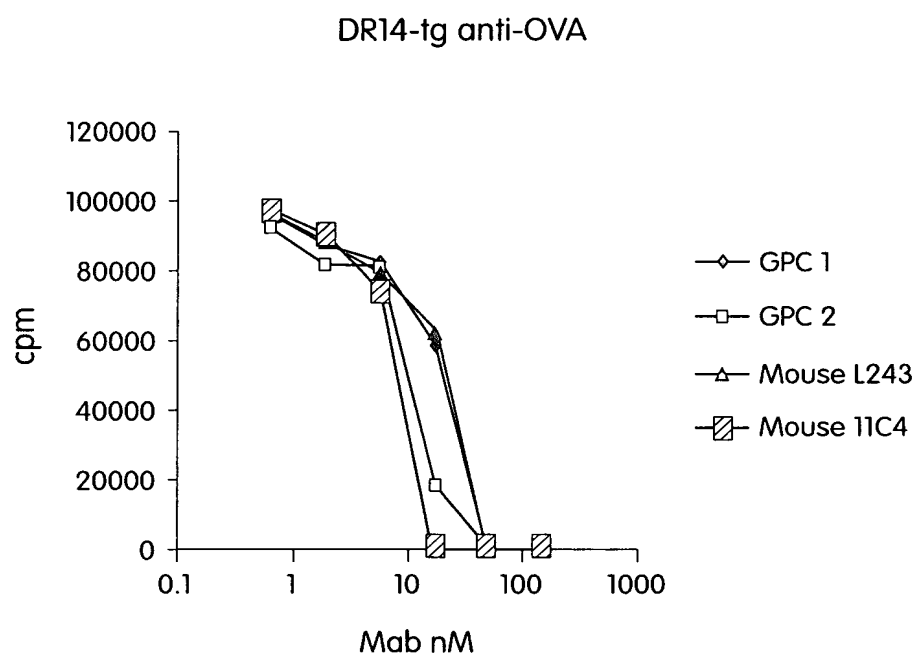


Fig. 9F

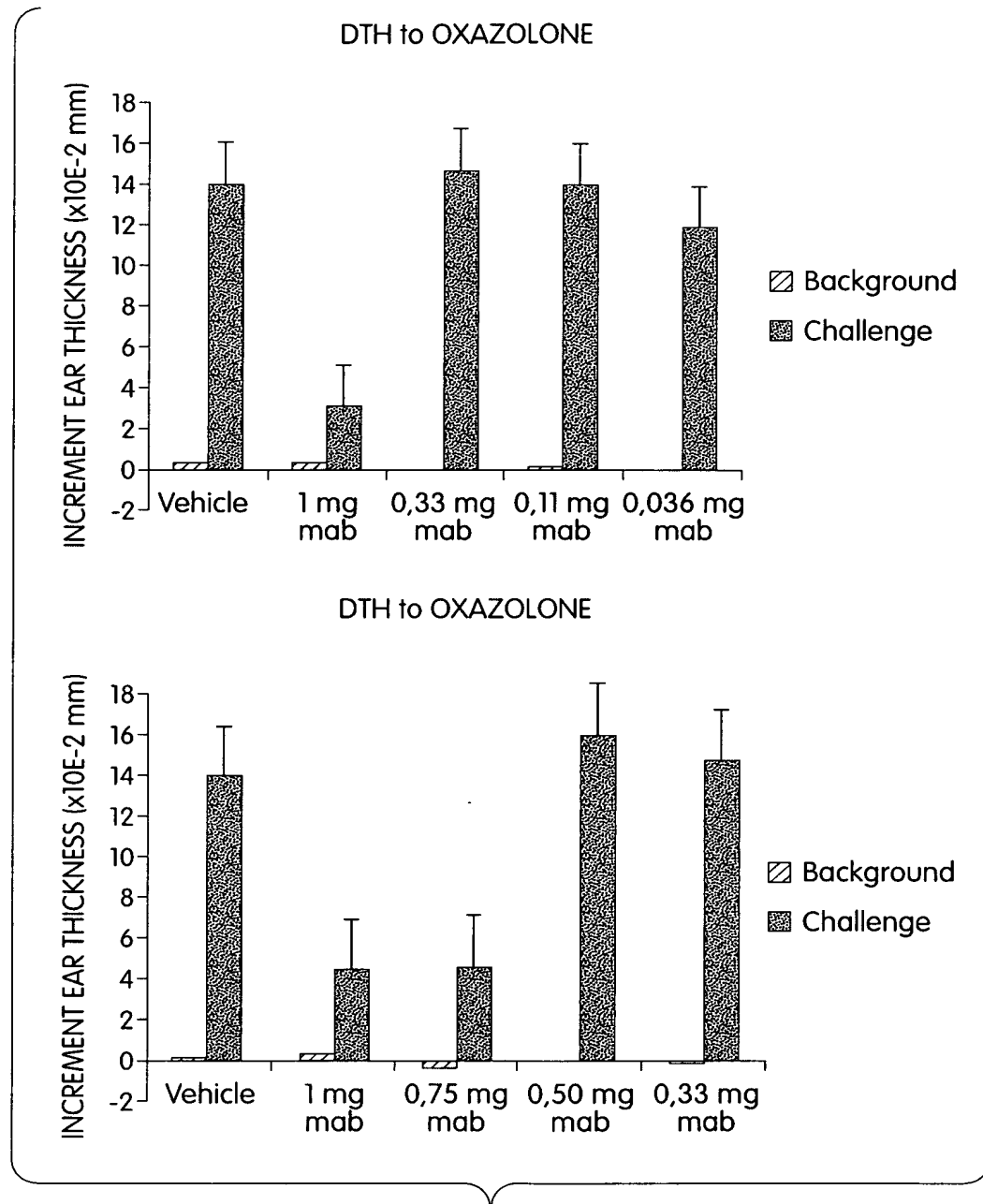
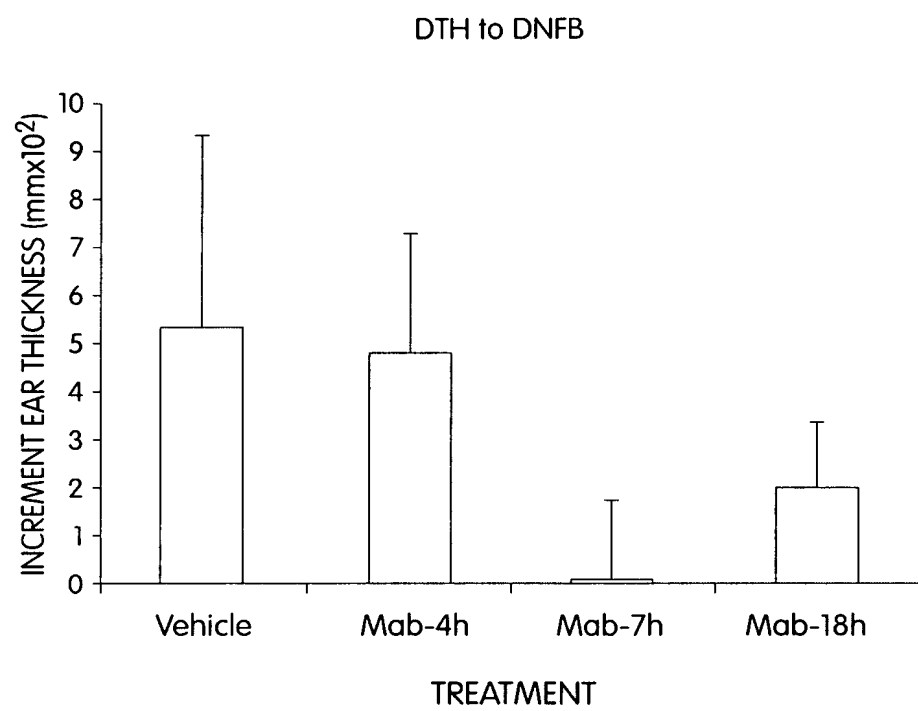


Fig. 9G

**Fig. 9H**

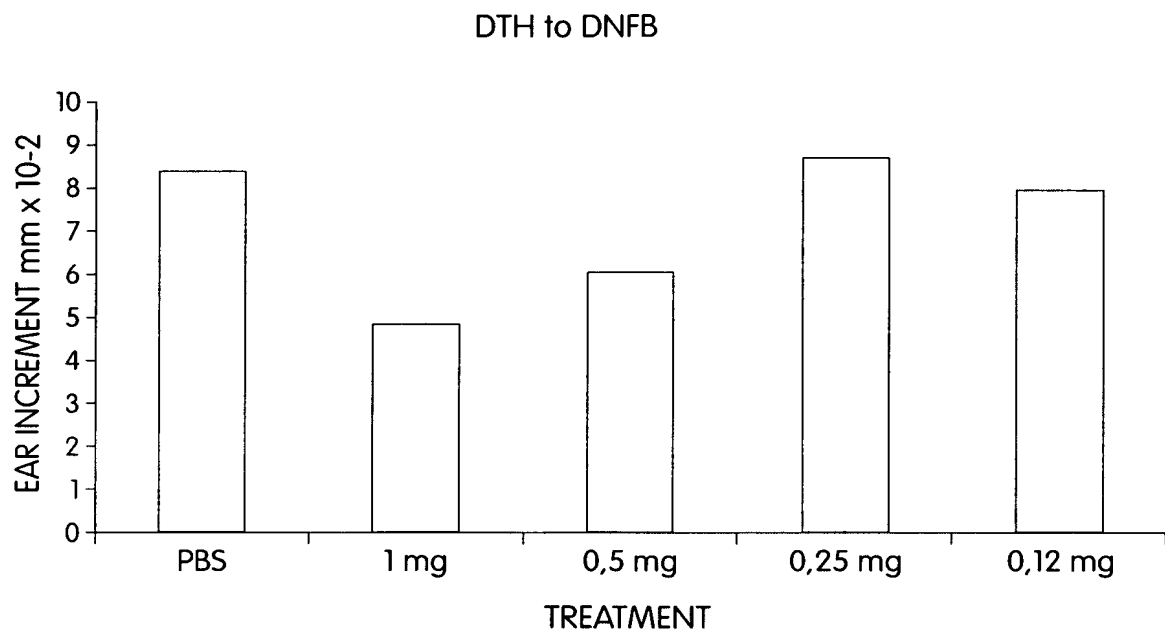


Fig. 9I

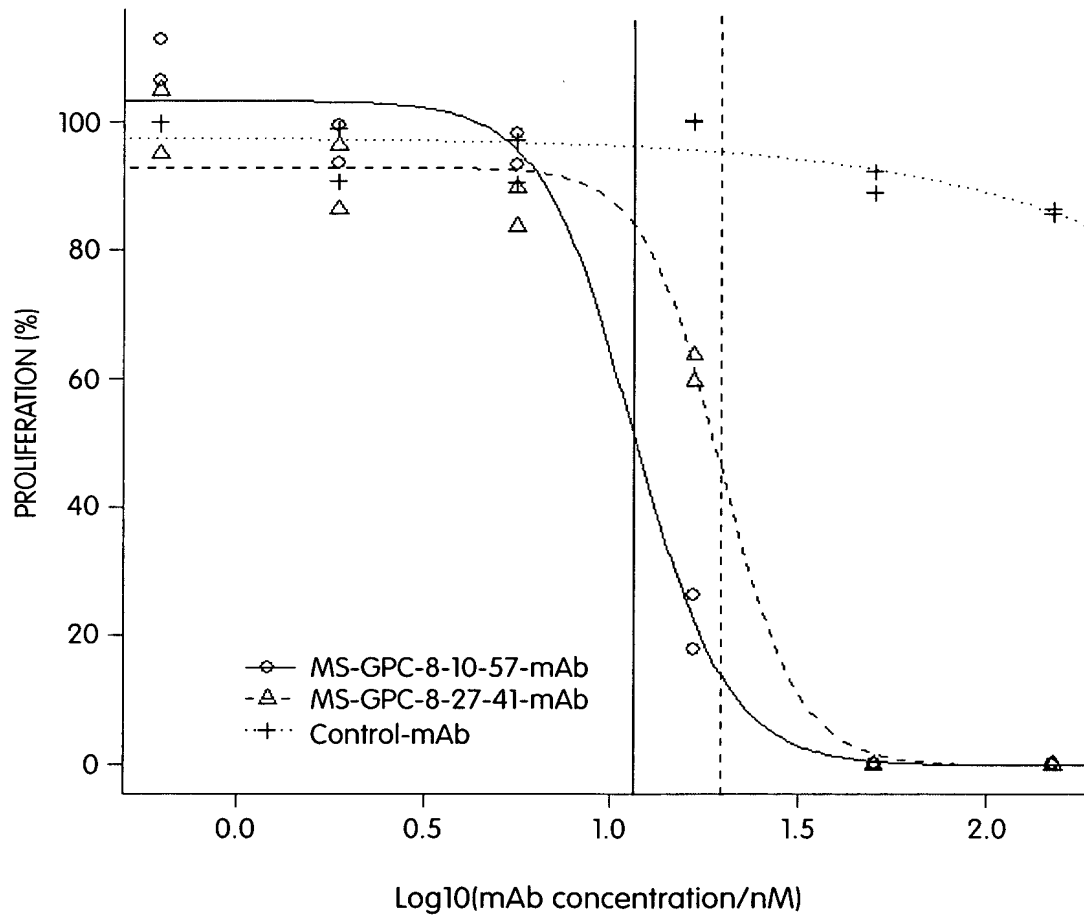


Fig. 10

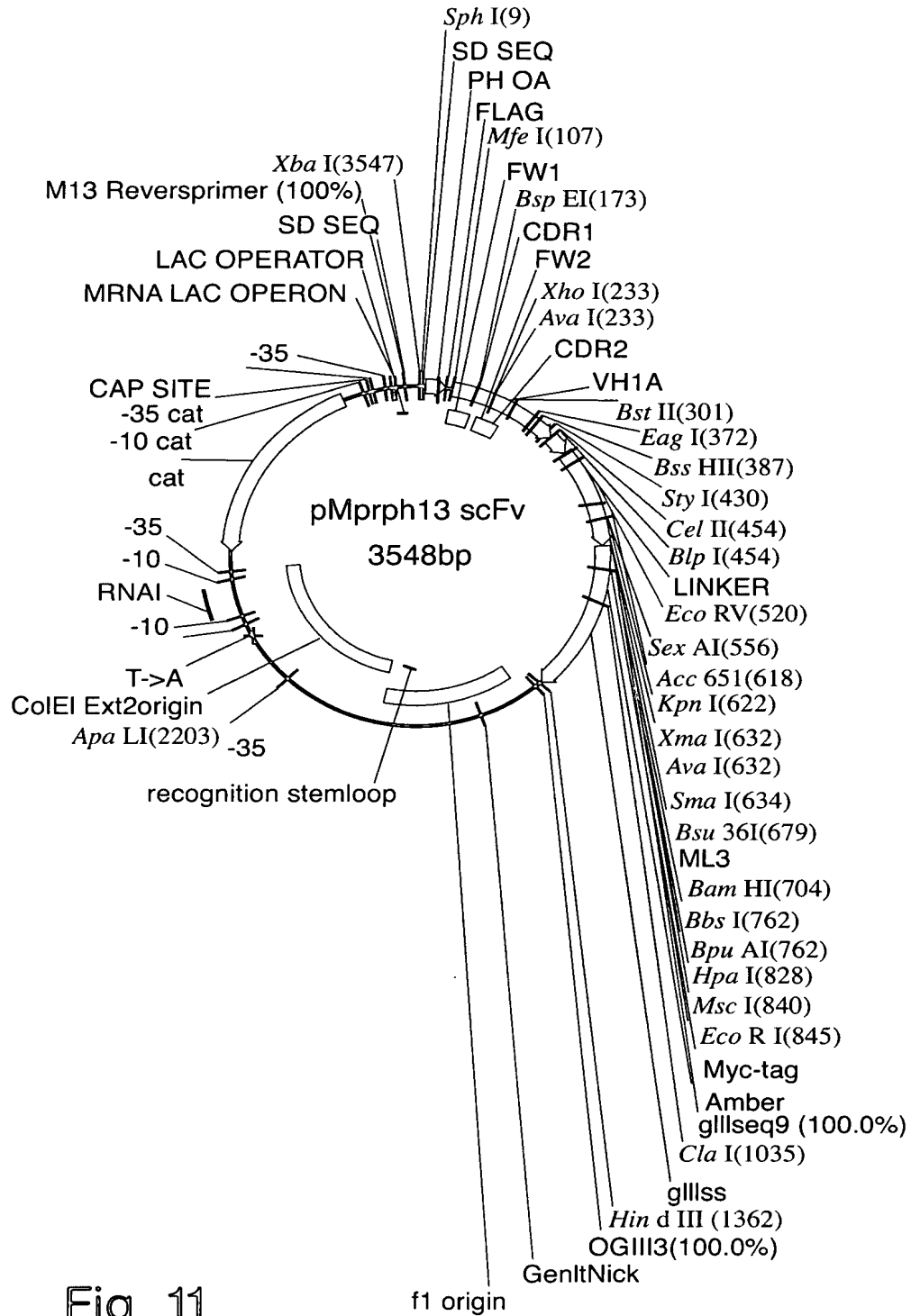


Fig. 11

```

XbaISphI
~~~~~
1  AGAGCATGCG TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC
   TCTCGTACGC ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG

51  ACTCTTACCG TTGCTCTTCA CCCCTGTTAC CAAAGCCGAC TACAAAGATG
   TGAGAATGGC AACGAGAAGT GGGGACAATG GTTTCGGCTG ATGTTTCTAC

      MfeI
      ~~~~~
101  AAGTGCAATT GGTTCAGTCT GGCGCGGAAG TGAAAAAACC GGGCAGCAGC
     TTCACGTAA CCAAGTCAGA CCGCGCCTTC ACTTTTTTGG CCCGTCGTCG

                BspEI
                ~~~~~
151  GTGAAAGTGA GCTGCAAAGC CTCCGGAGGC ACTTTTAGCA GCTATGCGAT
     CACTTTCAC TCGACGTTTCG GAGGCCTCCG TGAAAATCGT CGATACGCTA

                        XhoI
                        ~~~~~
                        AvaI
                        ~~~~~
201  TAGCTGGGTG CGCCAAGCCC CTGGGCAGGG TCTCGAGTGG ATGGGCGGCA
     ATCGACCCAC GCGGTTCCGG GACCCGTCCC AGAGCTCACC TACCCGCCGT

                                BstEII
                                ~~~~~
251  TTATTCCGAT TTTTGGCACG GCGAACTACG CGCAGAAGTT TCAGGGCCGG
     AATAAGGCTA AAAACCGTGC CGCTTGATGC GCGTCTTCAA AGTCCCGGCC

      BstEII
      ~~~~~
301  GTGACCATTA CCGCGGATGA AAGCACCAGC ACCGCGTATA TGGAAGTGA
     CACTGGTAAT GGCGCCTACT TTCGTGGTCG TGGCGCATAT ACCTTGACTC

                        EagI
                        ~~~~~
                        BssHII
                        ~~~~~
351  CAGCCTGCGT AGCGAAGATA CGGCCGTGTA TTATTGCGCG CGTTATTATG
     GTCGGACGCA TCGCTTCTAT GCCGGCACAT AATAACGCGC GCAATAATAC

                                StyI
                                ~~~~~
401  ATCGTATGTA TAATATGGAT TATTGGGGCC AAGGCACCCT GGTGACGGTT
     TAGCATACAT ATTATACCTA ATAACCCCGG TTCCGTGGGA CCACTGCCAA

      BlpI
      ~~~~~
      CelII
      ~~~~~
451  AGCTCAGCGG GTGGCGGTTC TGGCGGCGGT GGGAGCGGTG GCGGTGGTTC

```

Fig. 11 (cont.)

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TCGAGTCGCC CACCGCCAAG ACCGCCGCCA CCCTCGCCAC CGCCACCAAG

      EcoRV
      ~~~~~~
501  TGGCGGTGGT GGTTCGATA TCGAACTGAC CCAGCCGCCT TCAGTGAGCG
      ACCGCCACCA CCAAGGCTAT AGCTTGACTG GGTCGGCGGA AGTCACTCGC

      SexAI
      ~~~~~~
551  TTGCACCAGG TCAGACCGCG CGTATCTCGT GTAGCGGCGA TGCGCTGGGC
      AACGTGGTCC AGTCTGGCGC GCATAGAGCA CATCGCCGCT ACGCGACCCG

      XmaI
      ~~~~~~
      KpnI
      ~~~~~~
      SmaI
      ~~~~~~
      Acc65I
      ~~~~~~
      AvaI
      ~~~~~~
601  GATAAATACG CGAGCTGGTA CCAGCAGAAA CCCGGGCAGG CGCCAGTTCT
      CTATTTATGC GCTCGACCAT GGTCGTCTTT GGGCCCCGTCC GCGGTCAAGA

      Bsu36I
      ~~~~~~
651  GGTGATTTAT GATGATTCTG ACCGTCCCTC AGGCATCCCG GAACGCTTTA
      CCACTAAATA CTAATAAGAC TGGCAGGGAG TCCGTAGGGC CTTGCGAAAT

      BamHI
      ~~~~~~
701  GCGGATCCAA CAGCGGCAAC ACCGCGACCC TGACCATTAG CGGCACTCAG
      CGCCTAGGTT GTCGCCGTTG TGGCGCTGGG ACTGGTAATC GCCGTGAGTC

      BpuAI
      ~~~~~~
      BbsI
      ~~~~~~
751  GCGGAAGACG AAGCGGATTA TTATTGCCAG AGCTATGACG CTCATATGCG
      CGCCTTCTGC TTCGCCTAAT AATAACGGTC TCGATACTGC GAGTATACGC

      HpaI
      ~~~~~~
      MscI
      ~~~~~~
      EcoRI
      ~~~~~~
801  TCCTGTGTTT GGCGGCGGCA CGAAGTTAAC CGTTCTTGGC CAGGAATTCTG
      AGGACACAAA CCGCCGCCGT GCTTCAATTG GCAAGAACCG GTCCTTAAGC

851  AGCAGAAGCT GATCTCTGAG GAGGATCTGA ACTAGGGTGG TGGCTCTGGT
      TCGTCTTCGA CTAGAGACTC CTCCTAGACT TGATCCCACC ACCGAGACCA

901  TCCGGTGATT TTGATTATGA AAAGATGGCA AACGCTAATA AGGGGGCTAT
      AGGCCACTAA AACTAATACT TTTCTACCGT TTGCGATTAT TCCCCGATA

      gIIIseq9 100.0%
      =====
951  GACCGAAAAT GCCGATGAAA ACGCGCTACA GTCTGACGCT AAAGGCAAAC

```

Fig. 11 (cont.)

```

CTGGCTTTTA CGGCTACTTT TGC GCGATGT CAGACTGCGA TTTCCGTTTG

                                ClaI
                                ~~~~~~
1001 TTGATTCTGT CGCTACTGAT TACGGTGCTG CTATCGATGG TTTCATTGGT
    AACTAAGACA GCGATGACTA ATGCCACGAC GATAGCTACC AAAGTAACCA

1051 GACGTTTCCG GCCTTGCTAA TGGTAATGGT GCTACTGGTG ATTTTGCTGG
    CTGCAAAGGC CGGAACGATT ACCATTACCA CGATGACCAC TAAAACGACC

1101 CTCTAATTCC CAAATGGCTC AAGTCGGTGA CGGTGATAAT TCACCTTTAA
    GAGATTAAGG GTTTACCGAG TTCAGCCACT GCCACTATTA AGTGGA AATT

1151 TGAATAATTT CCGTCAATAT TTACCTTCCC TCCCTCAATC GGTTGAATGT
    ACTTATTAAA GGCAGTTATA AATGGAAGGG AGGGAGTTAG CCAACTTACA

1201 CGCCCTTTTG TCTTTGGCGC TGGTAAACCA TATGAATTTT CTATTGATTG
    GCGGGAAAAAC AGAAACCGCG ACCATTGTTG ATACTTAAAA GATAACTAAC

1251 TGACAAAATA AACTTATTCC GTGGTGTCTT TCGGTTTCTT TTATATGTTG
    ACTGTTTTAT TTGAATAAGG CACCACAGAA ACGCAAAGAA AATATACAAC

1301 CCACCTTTAT GTATGTATTT TCTACGTTTG CTAACATACT GCGTAATAAG
    GGTGGAAATA CATAcataaa AGATGCAAAC GATTGTATGA CGCATTATTC

                                HindIII
                                ~~~~~~
1351 GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
    CTCAGAACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
                                OGIII3 100.0%
                                =====

1401 ACATTTTTTTT TGTCTGCCGT TTAATGAAAT TGTAACGTT AATATTTTGT
    TGTAACAAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

1451 TAAAATTTCG CTTAAATTTT TGTTAAATCA GCTCATTTTT TAACCAATAG
    ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC

1501 GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG
    CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

1551 GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG
    CAACTCACAA CAAGGTCAAA CCTTGTTCTC AGGTGATAAT TTCTTGCACC

1601 ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA
    TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

1651 CGAGAACCAT CACCCTAATC AAGTTTTTTT GGGTCGAGGT GCCGTAAAGC
    GCTCTTGGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCG

1701 ACTAAATCGG AACCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
    TGATTTAGCC TTGGGATTTC CCTCGGGGGC TAAATCTCGA ACTGCCCTT

```

Fig. 11 (cont.)

1751	AGCCGGCGAA TCGGCCGCTT	CGTGGCGAGA GCACCGCTCT	AAGGAAGGGA TTCCTTCCCT	AGAAAGCGAA TCTTTCGCTT	AGGAGCGGGC TCCTCGCCCC
1801	GCTAGGGCGC CGATCCC GCG	TGGCAAGTGT ACCGTTCACA	AGCGGTCACG TCGCCAGTGC	CTGCGCGTAA GACGCGCATT	CCACCACACC GGTGGTGTGG
1851	CGCCGCGCTT GCGGCGCGAA	AATGCGCCGC TTACGCGGCG	TACAGGGCGC ATGTCCC GCG	GTGCTAGCCA CACGATCGGT	TGTGAGCAAA ACACTCGTTT
1901	AGGCCAGCAA TCCGGTCGTT	AAGGCCAGGA TTCCGGTCCT	ACCGTAAAAA TGGCATTTTT	GGCCGCGTTG CCGGCGCAAC	CTGGCGTTTT GACCGCAAAA
1951	TCCATAGGCT AGGTATCCGA	CCGCCCCCCT GGCGGGGGGA	GACGAGCATC CTGCTCGTAG	ACAAAAATCG TGTTTTTAGC	ACGCTCAAGT TGCGAGTTCA
2001	CAGAGGTGGC GTCTCCACCG	GAAACCCGAC CTTTGGGCTG	AGGACTATAA TCCTGATATT	AGATACCAGG TCTATGGTCC	CGTTTCCCCC GCAAAGGGGG
2051	TGGAAGCTCC ACCTTCGAGG	CTCGTGCGCT GAGCACGCGA	CTCCTGTTCC GAGGACAAGG	GACCCTGCCG CTGGGACGGC	CTTACCGGAT GAATGGCCTA
2101	ACCTGTCCGC TGGACAGGCG	CTTTCTCCCT GAAAGAGGGA	TCGGGAAGCG AGCCCTTCGC	TGGCGCTTTC ACCGCGAAAG	TCATAGCTCA AGTATCGAGT
2151	CGCTGTAGGT GCGACATCCA	ATCTCAGTTC TAGAGTCAAG	GGTGTAGGTC CCACATCCAG	GTTGCTCCA CAAGCGAGGT	AGCTGGGCTG TCGACCCGAC
	<p style="text-align: center;">ApaI ~~~~~</p>				
2201	TGTGCACGAA ACACGTGCTT	CCCCCGTTC GGGGGGCAAG	AGTCCGACCG TCAGGCTGGC	CTGCGCCTTA GACGCGGAAT	TCCGGTAACT AGGCCATTGA
2251	ATCGTCTTGA TAGCAGAACT	GTCCAACCCG CAGGTTGGGC	GTAAGACACG CATTCTGTGC	ACTTATCGCC TGAATAGCGG	ACTGGCAGCA TGACCGTCGT
2301	GCCACTGGTA CGGTGACCAT	ACAGGATTAG TGTCCTAATC	CAGAGCGAGG GTCTCGCTCC	TATGTAGGCG ATACATCCGC	GTGCTACAGA CACGATGTCT
2351	GTTCTTGAAG CAAGAACTTC	TGGTGGCCTA ACCACCGGAT	ACTACGGCTA TGATGCCGAT	CACTAGAAGA GTGATCTTCT	ACAGTATTTG TGTCATAAAC
2401	GTATCTGCGC CATAGACGCG	TCTGCTGTAG AGACGACATC	CCAGTTACCT GGTCAATGGA	TCGGAAAAAG AGCCTTTTTT	AGTTGGTAGC TCAACCATCG
2451	TCTTGATCCG AGAACTAGGC	GCAAACAAAC CGTTTGTTTG	CACCGCTGGT GTGGCGACCA	AGCGGTGGTT TCGCCACCAA	TTTTTGTTTG AAAAACAAAC
2501	CAAGCAGCAG GTTGTCGTC	ATTACGCGCA TAATGCGCGT	GAAAAAAAGG CTTTTTTTCC	ATCTCAAGAA TAGAGTTCTT	GATCCTTTGA CTAGGAAACT
2551	TCTTTTCTAC	GGGGTCTGAC	GCTCAGTGGA	ACGAAAATC	ACGTTAAGGG

Fig. 11 (cont.)

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	AGAAAAGATG	CCCCAGACTG	CGAGTCACCT	TGCTTTTGAG	TGCAATTCCC
2601	ATTTTGGTCA TAAAACCAGT	GATCTAGCAC CTAGATCGTG	CAGGCGTTTA GTCCGCAAAT	AGGGCACCAA TCCCGTGGTT	TAACTGCCTT ATTGACGGAA
2651	AAAAAAATTA TTTTTTTAAT	CGCCCCGCCC GCGGGGCGGG	TGCCACTCAT ACGGTGAGTA	CGCAGTACTG GCGTCATGAC	TTGTAATTCA AACATTAAGT
2701	TTAAGCATT AATTCGTAAG	TGCCGACATG ACGGCTGTAC	GAAGCCATCA CTTCGGTAGT	CAAACGGCAT GTTTGCCGTA	GATGAACCTG CTACTTGGAC
2751	AATCGCCAGC TTAGCGGTCG	GGCATCAGCA CCGTAGTCGT	CCTTGTCGCC GGAACAGCGG	TTGCGTATAA AACGCATATT	TATTTGCCCA ATAAACGGGT
2801	TAGTGAAAAC ATCACTTTTG	GGGGGCGAAG CCCCCGCTTC	AAGTTGTCCA TTCAACAGGT	TATTGGCTAC ATAACCGATG	GTTTAAATCA CAAATTTAGT
2851	AAACTGGTGA TTTGACCACT	AACTCACCCA TTGAGTGGGT	GGGATTGGCT CCCTAACCGA	GAGACGAAAA CTCTGCTTTT	ACATATTCTC TGTATAAGAG
2901	AATAAACCCCT TTATTTGGGA	TTAGGGAAAT AATCCCTTTA	AGGCCAGGTT TCCGGTCCAA	TTCACCGTAA AAGTGGCATT	CACGCCACAT GTGCGGTGTA
2951	CTTGCGAATA GAACGCTTAT	TATGTGTAGA ATACACATCT	AACTGCCGGA TTGACGGCCT	AATCGTCGTG TTAGCAGCAC	GTATTCACTC CATAAGTGAG
3001	CAGAGCGATG GTCTCGCTAC	AAAACGTTTC TTTTGCAAAG	AGTTTGCTCA TCAAACGAGT	TGGAAAACGG ACCTTTTGCC	TGTAACAAGG ACATTGTTCC
3051	GTGAACACTA CACTTGATGAT	TCCCATATCA AGGGTATAGT	CCAGCTCACC GGTCGAGTGG	GTCTTTCATT CAGAAAGTAA	GCCATACGGA CGGTATGCCT
3101	ACTCCGGGTG TGAGGCCAC	AGCATTCAATC TCGTAAGTAG	AGGCGGGCAA TCCGCCCGTT	GAATGTGAAT CTTACACTTA	AAAGGCCGGA TTTCCGGCCT
3151	TAAAACTTGT ATTTTGAACA	GCTTATTTTT CGAATAAAAA	CTTTACGGTC GAAATGCCAG	TTTAAAAAGG AAATTTTTC	CCGTAATATC GGCATTATAG
3201	CAGCTGAACG GTCGACTTGC	GTCTGGTTAT CAGACCAATA	AGGTACATTG TCCATGTAAAC	AGCAACTGAC TCGTTGACTG	TGAAATGCCT ACTTTACGGA
3251	CAAAATGTTC GTTTTACAAG	TTTACGATGC AAATGCTACG	CATTGGGATA GTAACCCTAT	TATCAACGGT ATAGTTGCCA	GGTATATCCA CCATATAGGT
3301	GTGATTTTTT CACTAAAAAA	TCTCCATTTT AGAGGTAAAA	AGCTTCCTTA TCGAAGGAAT	GCTCCTGAAA CGAGGACTTT	ATCTCGATAA TAGAGCTATT
3351	CTCAAAAAAT GAGTTTTTTA	ACGCCCGGTA TGCGGGCCAT	GTGATCTTAT CACTAGAATA	TTCATTATGG AAGTAATACC	TGAAAGTTGG ACTTTCAACC
3401	AACCTCACCC TTGGAGTGGG	GACGTCTAAT CTGCAGATTA	GTGAGTTAGC CACTCAATCG	TCACTCATT AGTGAGTAAT	GGCACCCAG CCGTGGGGTC

Fig. 11 (cont.)

```

3451  GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG
      CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC

           M13 Reverse primer 100.0%           XbaI
           =====
3501  ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTTCT
      TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAAAGA
  
```

Fig. 11 (cont.)

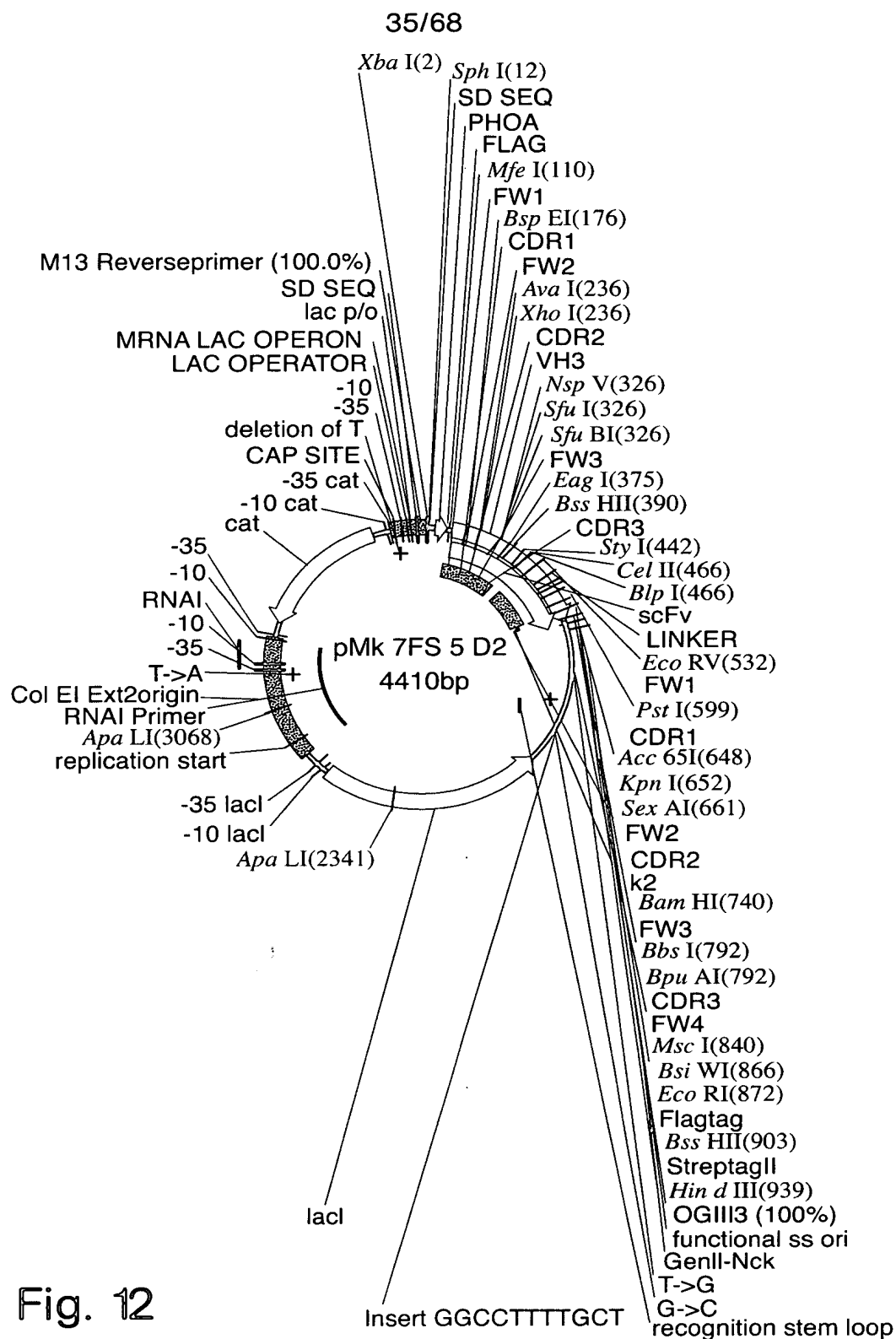


Fig. 12

```

      XbaI   SphI
      ~~~~~~
1   TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT
   AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

51  GGCACCTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG
   CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTGATGTTTC

      MfeI
      ~~~~~~
101 ATGAAGTGCA ATTGGTGGAA AGCGGCGGCG GCCTGGTGCA ACCGGGCGGC
   TACTTCACGT TAACCACCTT TCGCCGCCGC CGGACCACGT TGGCCCGCCG

      BspEI
      ~~~~~~
151 AGCCTGCGTC TGAGCTGCGC GGCCTCCGGA TTTACCTTTA GCAGCTATGC
   TCGGACGCAG ACTCGACGCG CCGGAGGCCT AAATGGAAAT CGTCGATACG

      XhoI
      ~~~~~~
      AvaI
      ~~~~~~
201 GATGAGCTGG GTGCGCCAAG CCCCTGGGAA GGGTCTCGAG TGGGTGAGCG
   CTACTCGACC CACGCGGTTC GGGGACCCTT CCCAGAGCTC ACCCACTCGC

251 CGATTAGCGG TAGCGGCGGC AGCACCTATT ATGCGGATAG CGTGAAAGGC
   GCTAATCGCC ATCGCCGCCG TCGTGATAAA TACGCCTATC GCACTTTCCG

      BstBI
      ~~~~~~
      SfuI
      ~~~~~~
      NspV
      ~~~~~~
301 CGTTTTACCA TTTCACGTGA TAATTCGAAA AACACCCTGT ATCTGCAAAT
   GCAAATGGT AAAGTGCACT ATTAAGCTTT TTGTGGGACA TAGACGTTTA

      EagI                      BssHII
      ~~~~~~                  ~~~~~~
351 GAACAGCCTG CGTGCGGAAG ATACGGCCGT GTATTATTGC GCGCGTGTTA
   CTTGTCGGAC GCACGCCTTC TATGCCGGCA CATAATAACG CGCGCACAAT

      StyI
      ~~~~~~
401 AGAAGCATTT TTCTCGTAAG AATTGTTTGT ATTATTGGGG CCAAGGCACC
   TCTTCGTAAA AAGAGCATTC TTAACCAAAC TAATAACCCC GGTTCGTTGG

```

Fig. 12 (cont.)

```

          BlnI
          ~~~~~
          CelII
          ~~~~~
451  CTGGTGACGG  TTAGCTCAGC  GGGTGGCGGT  TCTGGCGGCG  GTGGGAGCGG
     GACCACTGCC  AATCGAGTCG  CCCACCGCCA  AGACCGCCGC  CACCCTCGCC

                                EcoRV
                                ~~~~~
501  TGGCGGTGGT  TCTGGCGGTG  GTGGTTCCGA  TATCGTGATG  ACCCAGAGCC
     ACCGCCACCA  AGACCGCCAC  CACCAAGGCT  ATAGCACTAC  TGGGTCTCGG

                                                PstI
                                                ~~~~~
551  CACTGAGCCT  GCCAGTGACT  CCGGGCGAGC  CTGCGAGCAT  TAGCTGCAGA
     GTGACTCGGA  CGGTCACTGA  GGCCCGCTCG  GACGCTCGTA  ATCGACGTCT

                                                KpnI
                                                ~~~~~
                                                Acc65I
                                                ~~~~~
601  AGCAGCCAAA  GCCTGCTGCA  TAGCAACGGC  TATAACTATC  TGGATTGGTA
     TCGTCGGTTT  CGGACGACGT  ATCGTTGCCG  ATATTGATAG  ACCTAACCAT

KpnI
~~
Acc65I      SexAI
~~          ~~~~~
651  CCTTCAAAAA  CCAGGTCAAA  GCCCGCAGCT  ATTAATTTAT  CTGGGCAGCA
     GGAAGTTTTT  GGTCCAGTTT  CGGGCGTCGA  TAATTAAATA  GACCCGTCGT

                                BamHI
                                ~~~~~
701  ACCGTGCCAG  TGGGGTCCCG  GATCGTTTTA  GCGGCTCTGG  ATCCGGCACC
     TGGCACGGTC  ACCCCAGGGC  CTAGCAAAAT  CGCCGAGACC  TAGGCCGTGG

                                BpuAI
                                ~~~~~
                                BbsI
                                ~~~~~
751  GATTTTACCC  TGAAAATTAG  CCGTGTGGAA  GCTGAAGACG  TGGGCGTGTA
     CTAAAATGGG  ACTTTTAATC  GGCACACCTT  CGACTTCTGC  ACCCGCACAT

                                MscI
                                ~~~~~
801  TTATTGCCAG  CAGCATTATA  CCACCCCGCC  GACCTTTGGC  CAGGGTACGA
     AATAACGGTC  GTCGTAATAT  GGTGGGGCGG  CTGGAAACCG  GTCCCATGCT

```

Fig. 12-3

```

          BsiWI   EcoRI
          ~~~~~
851  AAGTTGAAAT TAAACGTACG GAATTCGACT ATAAAGATGA CGATGACAAA
    TTCAACTTTA ATTTGCATGC CTTAAGCTGA TATTTCTACT GCTACTGTTT

          BssHII                               HindIII
          ~~~~~                               ~~~~~
901  GGCGCGCCGT GGAGCCACCC GCAGTTTGAA AAATGATAAG CTTGACCTGT
    CCGCGCGGCA CCTCGGTGGG CGTCAAACCTT TTTACTATTC GAACTGGACA
                                   OGIII3 100.0%
                                   =====

951  GAAGTGAAAA ATGGCGCAGA TTGTGCGACA TTTTTTTTGT CTGCCGTTTA
    CTTCACTTTT TACCGCGTCT AACACGCTGT AAAAAAACA GACGGCAAAT
    OGIII3 100.0%
    =====

1001 ATTAAAGGGG GGGGGGGGCC GGCCTGGGGG GGGGTGTACA TGAAATTGTA
    TAATTTCCCC CCCCCCCC GG CCGGACCCCC CCCACATGT ACTTTAACAT

1051 AACGTTAATA TTTTGTTAAA ATTGCGGTTA AATTTTTGTT AAATCAGCTC
    TTGCAATTAT AAAACAATTT TAAGCGCAAT TTAAAAACAA TTTAGTCGAG

1101 ATTTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT AAATCAAAAG
    TAAAAAATTG GTTATCCGGC TTTAGCCGTT TTAGGGAATA TTTAGTTTTC

1151 AATAGACCGA GATAGGGTTG AGTGTGTGTT CAGTTTGGA CAAGAGTCCA
    TTATCTGGCT CTATCCCAAC TCACAACAAG GTCAAACCTT GTTCTCAGGT

1201 CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAAA CCGTCTATCA
    GATAATTTCT TGCACCTGAG GTTGCGAGTTT CCCGCTTTTT GGCAGATAGT

1251 GGGCGATGGC CCACTACGAG AACCATCACC CTAATCAAGT TTTTTGGGGT
    CCCGCTACCG GTGATGCTC TTGGTAGTGG GATTAGTTCA AAAAACCCCA

1301 CGAGGTGCCG TAAAGCACTA AATCGGAACC CTAAAGGGAG CCCCCGATTT
    GCTCCACGGC ATTTCTGTGAT TTAGCCTTGG GATTTCCTCT GGGGGCTAAA

1351 AGAGCTTGAC GGGGAAAGCC GGCGAACGTG GCGAGAAAGG AAGGGAAGAA
    TCTCGAACTG CCCCTTTCGG CCGCTTGACAC CGCTCTTTCC TTCCCTTCTT

1401 AGCGAAAGGA GCGGGCGCTA GGGCGCTGGC AAGTGTAGCG GTCACGCTGC
    TCGCTTTCCT CGCCCGCGAT CCCGCGACCG TTCACATCGC CAGTGCGACG

1451 GCGTAACCAC CACACCCGCC GCGCTTAATG CGCCGCTACA GGGCGCGTGC
    CGCATTTGGTG GTGTGGGCGG CGCGAATTAC GCGGCGATGT CCCGCGCACG

```

Fig. 12 (cont.)

```

1501 TAGACTAGTG TTTAAACCGG ACCGGGGGGG GGCTTAAGTG GGCTGCAAAA
    ATCTGATCAC AAATTTGGCC TGGCCCCCCC CCGAATTCAC CCGACGTTTT

1551 CAAAACGGCC TCCTGTCAGG AAGCCGCTTT TATCGGGTAG CCTCACTGCC
    GTTTTGCCGG AGGACAGTCC TTCGGCGAAA ATAGCCCATC GGAGTGACGG

1601 CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GCTGCATCAG TGAATCGGCC
    GCGAAAGGTC AGCCCTTTGG ACAGCACGGT CGACGTAGTC ACTTAGCCGG

1651 AACGCGCGGG GAGAGGCGGT TTGCGTATTG GGAGCCAGGG TGGTTTTTCT
    TTGCGCGCCC CTCTCCGCCA AACGCATAAC CCTCGGTCCC ACCAAAAAGA

1701 TTTCACCAGT GAGACGGGCA ACAGCTGATT GCCCTTCACC GCCTGGCCCT
    AAAGTGGTCA CTCTGCCCCG TGTCGACTAA CGGGAAGTGG CGGACCGGGA

1751 GAGAGAGTTG CAGCAAGCGG TCCACGCTGG TTTGCCCCAG CAGGCGAAAA
    CTCTCTCAAC GTCGTTTCGCC AGGTGCGACC AAACGGGGTC GTCCGCTTTT

1801 TCCTGTTTGA TGGTGGTCAG CGGCGGGATA TAACATGAGC TGTCTCGGT
    AGGACAAACT ACCACCAGTC GCCGCCCTAT ATTGTACTCG ACAGGAGCCA

1851 ATCGTCGTAT CCCACTACCG AGATGTCCGC ACCAACGCGC AGCCCGGACT
    TAGCAGCATA GGGTGATGGC TCTACAGGCG TGGTTGCGCG TCGGGCCTGA

1901 CGGTAATGGC ACGCATTGCG CCCAGCGCCA TCTGATCGTT GGCAACCAGC
    GCCATTACCG TGCCTAACGC GGGTCGCGGT AGACTAGCAA CCGTTGGTCG

1951 ATCGCAGTGG GAACGATGCC CTCATTGAGC ATTTGTCATGG TTTGTTGAAA
    TAGCGTCACC CTTGCTACGG GAGTAAGTCG TAAACGTACC AAACAACTTT

2001 ACCGGACATG GCACTCCAGT CGCCTTCCCG TTCCGCTATC GGCTGAATTT
    TGGCCTGTAC CGTGAGGTCA GCGGAAGGGC AAGGCGATAG CCGACTTAAA

2051 GATTGCGAGT GAGATATTTA TGCCAGCCAG CCAGACGCAG ACGCGCCGAG
    CTAACGCTCA CTCTATAAAT ACGGTCGGTC GGTCTGCGTC TCGCGGGCTC

2101 ACAGAACTTA ATGGGCCAGC TAACAGCGCG ATTTGCTGGT GGCCCAATGC
    TGTCTTGAAT TACCCGGTCG ATTGTGCGCG TAAACGACCA CCGGGTTACG

2151 GACCAGATGC TCCACGCCCCA GTCGCGTACC GTCCTCATGG GAGAAAATAA
    CTGGTCTACG AGGTGCGGGT CAGCGCATGG CAGGAGTACC CTCTTTTATT

2201 TACTGTTGAT GGGTGTCTGG TCAGAGACAT CAAGAAATAA CGCCGGAACA
    ATGACAATA CCCACAGACC AGTCTCTGTA GTTCTTTATT GCGGCCTTGT

2251 TTAGTGCAGG CAGCTTCCAC AGCAATAGCA TCCTGGTCAT CCAGCGGATA
    AATCACGTCC GTCGAAGGTG TCGTTATCGT AGGACCAGTA GGTGCGCTAT

```

ApaLI
~~~~~

Fig. 12 (cont.)

|      |                           |                           |                           |                          |                           |
|------|---------------------------|---------------------------|---------------------------|--------------------------|---------------------------|
| 2301 | GTAAATAATC<br>CAATTATTAG  | AGCCCACTGA<br>TCGGGTGACT  | CACGTTGCGC<br>GTGCAACGCG  | GAGAAGATTG<br>CTCTTCTAAC | TGCACCGCCG<br>ACGTGGCGGC  |
| 2351 | CTTTACAGGC<br>GAAATGTCCG  | TTCGACGCCG<br>AAGCTGCGGC  | CTTCGTTCTA<br>GAAGCAAGAT  | CCATCGACAC<br>GGTAGCTGTG | GACCACGCTG<br>CTGGTGCGAC  |
| 2401 | GCACCCAGTT<br>CGTGGGTCAA  | GATCGGCGCG<br>CTAGCCGCGC  | AGATTTAATC<br>TCTAAATTAG  | GCCGCGACAA<br>CGGCGCTGTT | TTTGCAGCGG<br>AAACGCTGCC  |
| 2451 | CGCGTGCAAG<br>GCGCACGTCC  | GCCAGACTGG<br>CGGTCTGACC  | AGGTGGCAAC<br>TCCACCGTTG  | GCCAATCAGC<br>CGGTTAGTCG | AACGACTGTT<br>TTGCTGACAA  |
| 2501 | TGCCCCGCCAG<br>ACGGGCGGTC | TTGTTGTGCC<br>AACAACACGG  | ACGCGGTTAG<br>TGCGCCAATC  | GAATGTAATT<br>CTTACATTAA | CAGCTCCGCC<br>GTGAGGCGG   |
| 2551 | ATCGCCGCTT<br>TAGCGGCGAA  | CCACTTTTTTC<br>GGTGAAAAAG | CCGCGTTTTTC<br>GGCGCAAAAG | GCAGAAACGT<br>CGTCTTTGCA | GGCTGGCCTG<br>CCGACCGGAC  |
| 2601 | GTTCAACACG<br>CAAGTGGTGC  | CGGGAAACGG<br>GCCCTTTGCC  | TCTGATAAGA<br>AGACTATTCT  | GACACCGGCA<br>CTGTGGCCGT | TACTCTGCGA<br>ATGAGACGCT  |
| 2651 | CATCGTATAA<br>GTAGCATATT  | CGTTACTGGT<br>GCAATGACCA  | TTCACATTCA<br>AAGTGTAAGT  | CCACCCTGAA<br>GGTGGGACTT | TTGACTCTCT<br>AACTGAGAGA  |
| 2701 | TCCGGGCGCT<br>AGGCCCGCGA  | ATCATGCCAT<br>TAGTACGGTA  | ACC GCGAAAG<br>TGGCGCTTTC | GTTTTGCGCC<br>CAAAACGCGG | ATTCGATGCT<br>TAAGCTACGA  |
| 2751 | AGCCATGTGA<br>TCGGTACACT  | GCAAAAGGCC<br>CGTTTTCCGG  | AGCAAAAGGC<br>TCGTTTTCCG  | CAGGAACCGT<br>GTCCTTGGA  | AAAAAGGCCG<br>TTTTTCCGGC  |
| 2801 | CGTTGCTGGC<br>GCAACGACCG  | GTTTTTCCAT<br>CAAAAAGGTA  | AGGCTCCGCC<br>TCCGAGGCGG  | CCCCTGACGA<br>GGGGACTGCT | GCATCACAAA<br>CGTAGTGTTT  |
| 2851 | AATCGACGCT<br>TTAGCTGCGA  | CAAGTCAGAG<br>GTTCACTCTC  | GTGGCGAAAC<br>CAACGCTTTG  | CCGACAGGAC<br>GGCTGTCCTG | TATAAAGATA<br>ATATTTCTAT  |
| 2901 | CCAGGCGTTT<br>GGTCCGCAAA  | CCCCCTGGAA<br>GGGGGACCTT  | GCTCCCTCGT<br>CGAGGGAGCA  | GCGCTCTCCT<br>CGCGAGAGGA | GTTCCGACCC<br>CAAGGCTGGG  |
| 2951 | TGCCGCTTAC<br>ACGGCGAATG  | CGGATACCTG<br>GCCTATGGAC  | TCCGCCTTTC<br>AGGCGGAAAG  | TCCCTTCGGG<br>AGGGAAGCCC | AAGCGTGGCG<br>TTGCGACCGC  |
| 3001 | CTTTCTCATA<br>GAAAGAGTAT  | GCTCACGCTG<br>CGAGTGCGAC  | TAGGTATCTC<br>ATCCATAGAG  | AGTTCGGTGT<br>TCAAGCCACA | AGGTCGTTTCG<br>TCCAGCAAGC |

ApaLI

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3051	CTCCAAGCTG GAGGTTTCGAC	GGCTGTGTGC CCGACACACG	ACGAACCCCC TGCTTGGGGG	CGTTCAGCCC GCAAGTCGGG	GACCGCTGCG CTGGCGACGC
3101	CCTTATCCGG GGAATAGGCC	TAAGTATCGT ATTGATAGCA	CTTGAGTCCA GAACTCAGGT	ACCCGCTAAG TGGGCCATTC	ACACGACTTA TGTGCTGAAT

Fig. 12 (cont.)

3151	TCGCCACTGG AGCGGTGACC	CAGCAGCCAC GTCGTCGGTG	TGGTAACAGG ACCATTGTCC	ATTAGCAGAG TAATCGTCTC	CGAGGTATGT GCTCCATACA
3201	AGGCGGTGCT TCCGCCACGA	ACAGAGTTCT TGTCTCAAGA	TGAAGTGGTG ACTTCACCAC	GCCTAACTAC CGGATTGATG	GGCTACACTA CCGATGTGAT
3251	GAAGAACAGT CTTCTTGTC	ATTTGGTATC TAAACCATAG	TGCGCTCTGC ACGCGAGACG	TGTAGCCAGT ACATCGGTCA	TACCTTCGGA ATGGAAGCCT
3301	AAAAGAGTTG TTTTCTCAAC	GTAGCTCTTG CATCGAGAAC	ATCCGGCAAA TAGGCCGTTT	CAAACCACCG GTTTGGTGGC	CTGGTAGCGG GACCATCGCC
3351	TGGTTTTTTTT ACCAAAAAAA	GTTTGCAAGC CAAACGTTTC	AGCAGATTAC TCGTCTAATG	GCGCAGAAAA CGCGTCTTTT	AAAGGATCTC TTTCCTAGAG
3401	AAGAAGATCC TTCTTCTAGG	TTTGATCTTT AAACTAGAAA	TCTACGGGGT AGATGCCCCA	CTGACGCTCA GACTGCGAGT	GTGGAACGAA CACCTTGCTT
3451	AACTCACGTT TTGAGTGCAA	AAGGGATTTT TTCCCTAAAA	GGTCAGATCT CCAGTCTAGA	AGCACCAGGC TCGTGGTCCG	GTTTAAGGGC CAAATTCCCC
3501	ACCAATAACT TGGTTATTGA	GCCTTAAAAA CGGAATTTTT	AATTACGCCC TTAATGCGGG	CGCCCTGCCA GCGGGACGGT	CTCATCGCAG GAGTAGCGTC
3551	TACTGTTGTA ATGACAACAT	ATTCATTAAG TAAGTAATTC	CATTCTGCCG GTAAGACGGC	ACATGGAAGC TGTACCTTCG	CATCACAAAC GTAGTGTTTG
3601	GGCATGATGA CCGTACTACT	ACCTGAATCG TGGACTTAGC	CCAGCGGCAT GGTCGCCGTA	CAGCACCTTG GTCGTGGAAC	TCGCCTTGCG AGCGGAACGC
3651	TATAATATTT ATATTATAAA	GCCCATAGTG CGGGTATCAC	AAAACGGGGG TTTTGCCCCC	CGAAGAAGTT GCTTCTTCAA	GTCCATATTG CAGGTATAAC
3701	GCTACGTTTA CGATGCAAAT	AATCAAAACT TTAGTTTTGA	GGTGAAACTC CCACTTTGAG	ACCCAGGGAT TGGGTCCCTA	TGGCTGAGAC ACCGACTCTG
3751	GAAAAACATA CTTTTTGTAT	TTCTCAATAA AAGAGTTATT	ACCCTTTAGG TGGGAAATCC	GAAATAGGCC CTTTATCCGG	AGGTTTTTCAC TCCAAAAGTG
3801	CGTAACACGC GCATTGTGCG	CACATCTTGC GTGTAGAACG	GAATATATGT CTTATATACA	GTAGAAACTG CATCTTTGAC	CCGGAAATCG GGCCTTTAGC
3851	TCGTGGTATT AGCACCATAA	CACTCCAGAG GTGAGGTCTC	CGATGAAAAC GCTACTTTTG	GTTTCAGTTT CAAAGTCAAA	GCTCATGGAA CGAGTACCTT
3901	AACGGTGTA TTGCCACATT	CAAGGGTGAA GTTCCCACTT	CACTATCCCA GTGATAGGGT	TATCACCAGC ATAGTGGTCG	TCACCGTCTT AGTGGCAGAA
3951	TCATTGCCAT AGTAACGGTA	ACGGAACCTC TGCCTTGAGG	GGGTGAGCAT CCCACTCGTA	TCATCAGGCG AGTAGTCCGC	GGCAAGAATG CCGTTCTTAC

Fig. 12 (cont.)

```

4001  TGAATAAAGG  CCGGATAAAA  CTTGTGCTTA  TTTTCTTTA  CGGTCTTTAA
      ACTTATTTCC  GGCCTATTTT  GAACACGAAT  AAAAAGAAAT  GCCAGAAATT

4051  AAAGGCCGTA  ATATCCAGCT  GAACGGTCTG  GTTATAGGTA  CATTGAGCAA
      TTTCCGGCAT  TATAGGTCGA  CTTGCCAGAC  CAATATCCAT  GTAACTCGTT

4101  CTGACTGAAA  TGCCTCAAAA  TGTTCTTTAC  GATGCCATTG  GGATATATCA
      GACTGACTTT  ACGGAGTTTT  ACAAGAAATG  CTACGGTAAC  CCTATATAGT

4151  ACGGTGGTAT  ATCCAGTGAT  TTTTTTCTCC  ATTTTAGCTT  CCTTAGCTCC
      TGCCACCATA  TAGGTCACTA  AAAAAAGAGG  TAAAATCGAA  GGAATCGAGG

4201  TGAAAAATCTC  GATAACTCAA  AAAATACGCC  CGGTAGTGAT  CTTATTTTCAT
      ACTTTTAGAG  CTATTGAGTT  TTTTATGCGG  GCCATCACTA  GAATAAAGTA

4251  TATGGTGAAA  GTTGGAACCT  CACCCGACGT  CTAATGTGAG  TTAGCTCACT
      ATACCACTTT  CAACCTTGGA  GTGGGCTGCA  GATTACACTC  AATCGAGTGA

4301  CATTAGGCAC  CCCAGGCTTT  ACACTTTATG  CTTCCGGCTC  GTATGTTGTG
      GTAATCCGTG  GGGTCCGAAA  TGTGAAATAC  GAAGGCCGAG  CATAACAACAC

                                     M13 Reverse primer 100.0%
                                     =====
4351  TGGAATTGTG  AGCGGATAAC  AATTTACAC  AGGAAACAGC  TATGACCATG
      ACCTTAACAC  TCGCCTATTG  TTAAAGTGTG  TCCTTTGTCTG  ATACTGGTAC

4401  ATTACGAATT
      TAATGCTTAA

```

Fig. 12 (cont.)

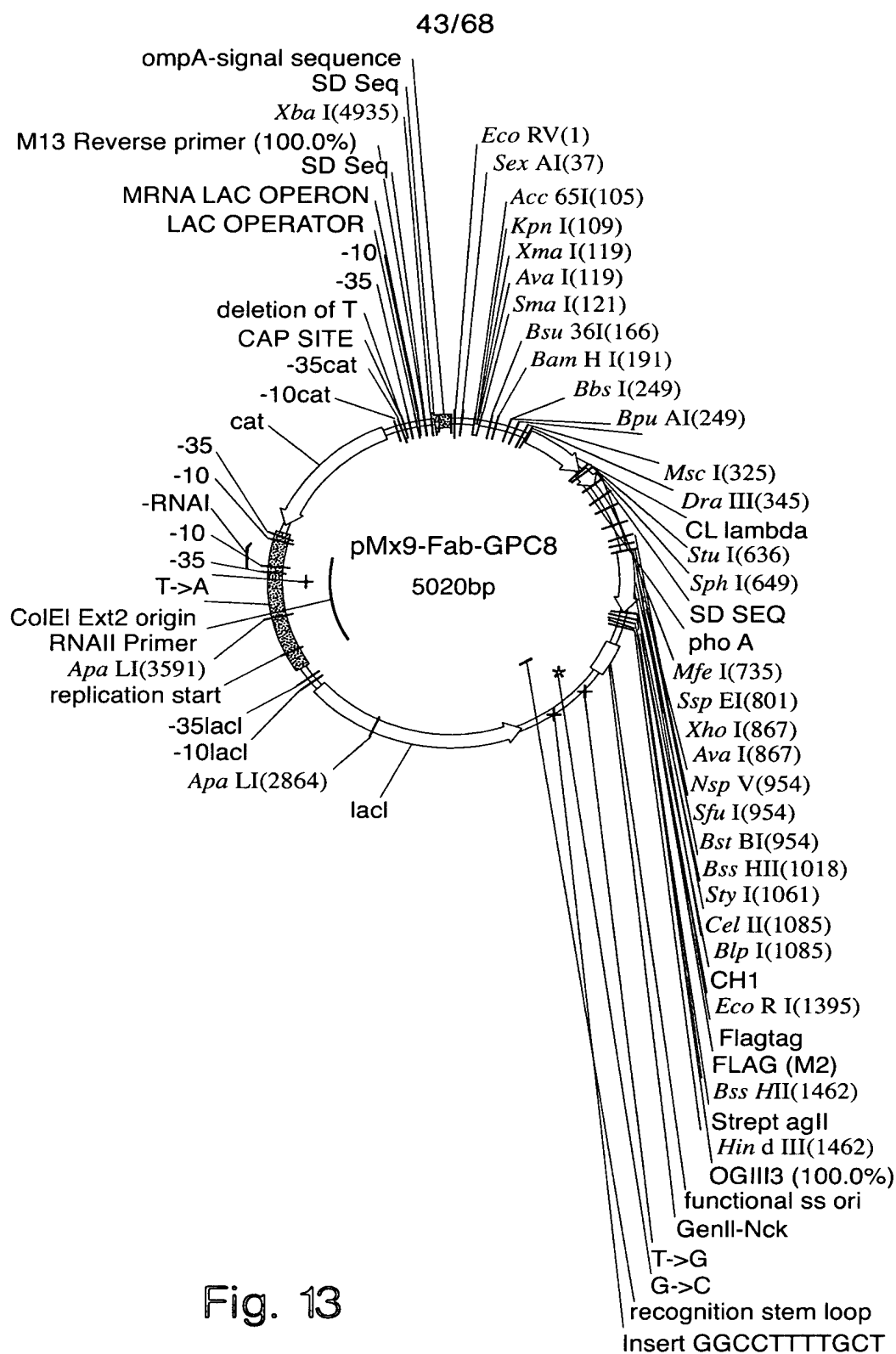


Fig. 13

	EcoRV ~~~		SexAI ~~~~~	
1	ATCGTGCTGA TAGCACGACT	CCCAGCCGCC GGGTCGGCGG	TTCAGTGAGT AAGTCACTCA	GGCGCACCAG CCGCGTGGTC
51	GACCATCTCG CTGGTAGAGC	TGTAGCGGCA ACATCGCCGT	GCAGCAGCAA CGTCGTCGTT	CATTGGCAGC GTAACCGTCG
		XmaI ~~~~~		
	KpnI ~~~~~	SmaI ~~~~~		
	Acc65I ~~~~~	AvaI ~~~~~		
101	GCTGGTACCA CGACCATGGT	GCAGTTGCCC CGTCAACGGG	GGGACGGCGC CCCTGCCGCG	CGAAACTGCT GCTTTGACGA
		Bsu36I ~~~~~	BamHI ~~~~~	
151	AACAACCAGC TTGTTGGTCG	GTCCCTCAGG CAGGGAGTCC	CGTGCCGGAT GCACGGCCTA	CGTTTTAGCG GCAAAATCGC
			BpuAI ~~~~~	
			BbsI ~~~~~	
201	CGGCACCAGC GCCGTGGTCG	GCGAGCCTTG CGCTCGGAAC	CGATTACGGG GCTAATGCCC	CCTGCAAAGC GGACGTTTCG
		Bsu36I ~~~~~		
251	CGGATTATTA GCCTAATAAT	TTGCCAGAGC AACGGTCTCG	TATGACATGC ATACTGTACG	CTCAGGCTGT GAGTCCGACA
		MscI ~~~~~	DraIII ~~~~~	
301	GGCACGAAGT CCGTGCTTCA	TTAACCGTTC AATTGGCAAG	TTGGCCAGCC AACC GGTCGG	GAAAGCCGCA CTTTCGGCGT
351	CGCTGTTTCC GCGACAAAGG	GCCGAGCAGC CGGCTCGTCG	GAAGAATTGC CTTCTTAACG	AGGCGAACAA TCCGCTTGTT
401	GTGTGCCTGA CACACGGACT	TTAGCGACTT AATCGCTGAA	TTATCCGGGA AATAGGCCCT	GCCGTGACAG CGGCACTGTC
451	GGCAGATAGC CCGTCTATCG	AGCCCCGTCA TCGGGGCAGT	AGGCGGGAGT TCCGCCCTCA	GGAGACCACC CCTCTGGTGG
501	AACAAAGCAA TTGTTTCGTT	CAACAAGTAC GTTGTTCATG	GCGGCCAGCA CGCCGGTCGT	GCTATCTGAG CGATAGACTC
				CCTGACGCCCT GGACTGCGGA

Fig. 13 (cont.)

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551  GAGCAGTGGG AGTCCCACAG AAGCTACAGC TGCCAGGTCA CGCATGAGGG
      CTCGTCACCT TCAGGGTGTC TTCGATGTCG ACGGTCCAGT GCGTACTCCC

                                     StuI           SphI
                                     ~~~~~~           ~~~~~~
601  GAGCACCGTG GAAAAAACCG TTGCGCCGAC TGAGGCCTGA TAAGCATGCG
      CTCGTGGCAC CTTTTTTGGC AACGCGGCTG ACTCCGGACT ATTCGTACGC

651  TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC ACTCTTACCG
      ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG TGAGAATGGC

                                     MfeI
                                     ~~~~~~
701  TTGCTCTTCA CCCCTGTTAC CAAAGCCCAG GTGCAATTGA AAGAAAGCGG
      AACGAGAAGT GGGGACAATG GTTTCGGGTC CACGTTAACT TTCTTTCGCC

                                     BspEI
                                     ~~~~~~
751  CCCGGCCCTG GTGAAACCGA CCCAAACCCT GACCCTGACC TGTACCTTTT
      GGGCCGGGAC CACTTTGGCT GGGTTTGGGA CTGGGACTGG ACATGGAAAA

BspEI
~~~~~
801  CCGGATTTAG CCTGTCCACG TCTGGCGTTG GCGTGGGCTG GATTGCGCCAG
      GGCCTAAATC GGACAGGTGC AGACCGCAAC CGCACCCGAC CTAAGCGGTC

                                     XhoI
                                     ~~~~~~
                                     AvaI
                                     ~~~~~~
851  CCGCCTGGGA AAGCCCTCGA GTGGCTGGCT CTGATTGATT GGGATGATGA
      GGCGGACCCT TTCGGGAGCT CACCGACCGA GACTAACTAA CCCTACTACT

901  TAAGTATTAT AGCACCAGCC TGAAAACGCG TCTGACCATT AGCAAAGATA
      ATTCATAATA TCGTGGTCGG ACTTTTGCGC AGACTGGTAA TCGTTTCTAT

      BstBI
      ~~~~~~
      SfuI
      ~~~~~~
      NspV
      ~~~~~~
951  CTTCGAAAAA TCAGGTGGTG CTGACTATGA CCAACATGGA CCCGGTGGAT
      GAAGCTTTTT AGTCCACCAC GACTGATACT GGTGTACCT GGGCCACCTA

                                     BssHII
                                     ~~~~~~
1001 ACGGCCACCT ATTATTGCGC GCGTTCTCCT CGTTATCGTG GTGCTTTTGA
      TGCCGGTGGA TAATAACGCG CGCAAGAGGA GCAATAGCAC CACGAAAACT

                                     BlpI

```

Fig. 13 (cont.)

	StyI ~~~~~			CelII ~~~~~	
1051	TTATTGGGGC AATAACCCCG	CAAGGCACCC GTTCCGTGGG	TGGTGACGGT ACCACTGCCA	TAGCTCAGCG ATCGAGTCGC	TCGACCAAAG AGCTGGTTTC
1101	GTCCAAGCGT CAGGTTGCGA	GTTTCCGCTG CAAAGGCGAC	GCTCCGAGCA CGAGGCTCGT	GCAAAAGCAC CGTTTTTCGTG	CAGCGGCGGC GTCGCCGCCG
1151	ACGGCTGCCC TGCCGACGGG	TGGGCTGCCT ACCCGACGGA	GGTTAAAGAT CCAATTTCTA	TATTTCCCGG ATAAAGGGCC	AACCAGTCAC TTGGTCAGTG
1201	CGTGAGCTGG GCACTCGACC	AACAGCGGGG TTGTCGCCCC	CGCTGACCAG GCGACTGGTC	CGGCGTGCAT GCCGCACGTA	ACCTTTCCGG TGGAAAGGCC
1251	CGGTGCTGCA GCCACGACGT	AAGCAGCGGC TTCGTCGCCG	CTGTATAGCC GACATATCGG	TGAGCAGCGT ACTCGTCGCA	TGTGACCGTG ACACTGGCAC
1301	CCGAGCAGCA GGCTCGTCGT	GCTTAGGCAC CGAATCCGTG	TCAGACCTAT AGTCTGGATA	ATTTGCAACG TAAACGTTGC	TGAACCATAA ACTTGGTATT
					EcoRI ~~~~~
1351	ACCGAGCAAC TGGCTCGTTG	ACCAAAGTGG TGGTTTCACC	ATAAAAAAGT TATTTTTTCA	GGAACCGAAA CCTTGGCTTT	AGCGAATTCG TCGCTTAAGC
			BssHII ~~~~~		
1401	ACTATAAAGA TGATATTCT	TGACGATGAC ACTGCTACTG	AAAGGCGCGC TTTCCGCGCG	CGTGGAGCCA GCACCTCGGT	CCCGCAGTTT GGGCGTCAAA
			HindIII ~~~~~		
1451	GAAAAATGAT CTTTTTACTA	AAGCTTGACC TTCGAACTGG	TGTGAAGTGA ACACTTCACT	AAAATGGCGC TTTTACCGCG	AGATTGTGCG TCTAACACGC
			OGIII3 100.0%		
			=====		
1501	ACATTTTTTT TGTAACAAAA	TGTCTGCCGT ACAGACGGCA	TTAATTAAAG AATTAATTTT	GGGGGGGGGG CCCCCCCCC	GCCGGCCTGG CGGCCGGACC
1551	GGGGGGGTGT CCCCCCCACA	ACATGAAATT TGTACTTTAA	GTAAACGTTA CATTTGCAAT	ATATTTTGTT TATAAAACAA	AAAATTCGCG TTTAAAGCGC
1601	TTAAATTTTT AATTTAAAAA	GTTAAATCAG CAATTTAGTC	CTCATTTTTT GAGTAAAAAA	AACCAATAGG TTGGTTATCC	CCGAAATCGG GGCTTTAGCC
1651	CAAAATCCCT GTTTTAGGGA	TATAAATCAA ATATTTAGTT	AAGAATAGAC TTCTTATCTG	CGAGATAGGG GCTCTATCCC	TTGAGTGTTG AACTCACAAAC
1701	TTCCAGTTTG AAGGTCAAAC	GAACAAGAGT CTTGTTCTCA	CCACTATTAA GGTGATAATT	AGAACGTGGA TCTTGCACCT	CTCCAACGTC GAGGTTGCAG

Fig. 13 (cont.)

1751	AAAGGGCGAA TTTCCCGCTT	AAACCGTCTA TTTGGCAGAT	TCAGGGCGAT AGTCCCCTA	GGCCCACTAC CCGGGTGATG	GAGAACCATC CTCTTGGTAG
1801	ACCCTAATCA TGGGATTAGT	AGTTTTTTTG TCAAAAAACC	GGTCGAGGTG CCAGCTCCAC	CCGTAAAGCA GGCATTTCGT	CTAAATCGGA GATTTAGCCT
1851	ACCCTAAAGG TGGGATTTCC	GAGCCCCCGA CTCGGGGGCT	TTTAGAGCTT AAATCTCGAA	GACGGGGAAA CTGCCCCCTT	GCCGGCGAAC CGGCCGCTTG
1901	GTGGCGAGAA CACCGCTCTT	AGGAAGGGAA TCCTTCCCTT	GAAAGCGAAA CTTTCGCTTT	GGAGCGGGCG CCTCGCCCCG	CTAGGGCGCT GATCCCGCGA
1951	GGCAAGTGTA CCGTTTACAT	GCGGTCACGC CGCCAGTGCG	TGCGCGTAAC ACGCGCATTG	CACCACACCC GTGGTGTGGG	GCCGCGCTTA CGGCGCGAAT
2001	ATGCGCCGCT TACGCGGCGA	ACAGGGCGCG TGTCCCGCGC	TGCTAGACTA ACGATCTGAT	GTGTTTAAAC CACAAATTTG	CGGACCGGGG GCCTGGCCCC
2051	GGGGGCTTAA CCCCCGAATT	GTGGGCTGCA CACCCGACGT	AAACAAAACG TTTGTTTTGC	GCCTCCTGTC CGGAGGACAG	AGGAAGCCGC TCCTTCGGCG
2101	TTTTATCGGG AAAATAGCCC	TAGCCTCACT ATCGGAGTGA	GCCCCTTTC CGGGCGAAAAG	CAGTCGGGAA GTCAGCCCTT	ACCTGTCTGT TGGACAGCAC
2151	CCAGCTGCAT GGTCGACGTA	CAGTGAATCG GTCACCTTAGC	GCCAACGCGC CGGTTGCGCG	GGGGAGAGGC CCCCCTCTCCG	GGTTTGCGTA CCAAACGCAT
2201	TTGGGAGCCA AACCCTCGGT	GGGTGGTTTT CCCACCAAAA	TCTTTTCACC AGAAAAGTGG	AGTGAGACGG TCACTCTGCC	GCAACAGCTG CGTTGTGCAC
2251	ATTGCCCTTC TAACGGGAAG	ACCGCCTGGC TGGCGGACCG	CCTGAGAGAG GGACTCTCTC	TTGCAGCAAG AACGTCGTTC	CGGTCCACGC GCCAGGTGCG
2301	TGGTTTGCCC ACCAAACGGG	CAGCAGGCGA GTCGTCCGCT	AAATCCTGTT TTTAGGACAA	TGATGGTGGT ACTACCACCA	CAGCGGCGGG GTCGCCGCC
2351	ATATAACATG TATATTGTAC	AGCTGTCCTC TCGACAGGAG	GGTATCGTCG CCATAGCAGC	TATCCCCTA ATAGGGTGAT	CCGAGATGTC GGCTCTACAG
2401	CGCACCAACG GCGTGGTTGC	CGCAGCCCGG GCGTCGGGCC	ACTCGGTAAT TGAGCCATTA	GGCACGCATT CCGTGCGTAA	GCGCCAGCG CGCGGGTCGC
2451	CCATCTGATC GGTAGACTAG	GTTGGCAACC CAACCGTTGG	AGCATCGCAG TCGTAGCGTC	TGGGAACGAT ACCCTTGCTA	GCCCTCATTC CGGGAGTAAG
2501	AGCATTTGCA TCGTAAACGT	TGGTTTGTG ACCAAACAAC	AAAACCGGAC TTTTGGCCTG	ATGGCACTCC TACCGTGAGG	AGTCGCCTTC TCAGCGGAAG
2551	CCGTTCCGCT GGCAAGGCGA	ATCGGCTGAA TAGCCGACTT	TTTGATTGCG AAACTAACGC	AGTGAGATAT TCACTCTATA	TTATGCCAGC AATACGGTCG

Fig. 13 (cont.)

2601	CAGCCAGACG GTCGGTCTGC	CAGACGCGCC GTCTGCGCGG	GAGACAGAAC CTCTGTCTTG	TTAATGGGCC AATTACCCGG	AGCTAACAGC TCGATTGTCG
2651	GCGATTTGCT CGCTAAACGA	GGTGGCCCAA CCACCGGGTT	TGCGACCAGA ACGCTGGTCT	TGCTCCACGC ACGAGGTGCG	CCAGTCGCGT GGTCAGCGCA
2701	ACCGTCCTCA TGGCAGGAGT	TGGGAGAAAA ACCCTCTTTT	TAATACTGTT ATTATGACAA	GATGGGTGTC CTACCCACAG	TGGTCAGAGA ACCAGTCTCT
2751	CATCAAGAAA GTAGTTCTTT	TAACGCCGGA ATTGCGGCCT	ACATTAGTGC TGTAATCACG	AGGCAGCTTC TCCGTCGAAG	CACAGCAATA GTGTCGTTAT
2801	GCATCCTGGT CGTAGGACCA	CATCCAGCGG GTAGGTCGCC	ATAGTTAATA TATCAATTAT	ATCAGCCCAC TAGTCGGGTG	TGACACGTTG ACTGTGCAAC

ApaLI

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|      |                          |                          |                          |                          |                          |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 2851 | CGCGAGAAGA<br>GCGCTCTTCT | TTGTGCACCG<br>AACACGTGGC | CCGCTTTACA<br>GGCGAAATGT | GGCTTCGACG<br>CCGAAGCTGC | CCGCTTCGTT<br>GGCGAAGCAA |
| 2901 | CTACCATCGA<br>GATGGTAGCT | CACGACCACG<br>GTGCTGGTGC | CTGGCACCCA<br>GACCGTGGGT | GTTGATCGGC<br>CAACTAGCCG | GCGAGATTTA<br>CGCTCTAAAT |
| 2951 | ATCGCCGCGA<br>TAGCGGCGCT | CAATTTGCGA<br>GTTAAACGCT | CGGCGCGTGC<br>GCCGCGCACG | AGGGCCAGAC<br>TCCCGGTCTG | TGGAGGTGGC<br>ACCTCCACCG |
| 3001 | AACGCCAATC<br>TTGCGGTTAG | AGCAACGACT<br>TCGTTGCTGA | GTTTGCCCGC<br>CAAACGGGCG | CAGTTGTTGT<br>GTCAACAACA | GCCACGCGGT<br>CGGTGCGCCA |
| 3051 | TAGGAATGTA<br>ATCCTTACAT | ATTCAGCTCC<br>TAAGTCGAGG | GCCATCGCCG<br>CGGTAGCGGC | CTTCCACTTT<br>GAAGGTGAAA | TTCCCGCGTT<br>AAGGGCGCAA |
| 3101 | TTCGCAGAAA<br>AAGCGTCTTT | CGTGGCTGGC<br>GCACCGACCG | CTGGTTCACC<br>GACCAAGTGG | ACGCGGGAAA<br>TGCGCCCTTT | CGGTCTGATA<br>GCCAGACTAT |
| 3151 | AGAGACACCG<br>TCTCTGTGGC | GCATACTCTG<br>CGTATGAGAC | CGACATCGTA<br>GCTGTAGCAT | TAACGTTACT<br>ATTGCAATGA | GGTTTCACAT<br>CCAAAGTGTA |
| 3201 | TCACCACCCT<br>AGTGGTGGGA | GAATTGACTC<br>CTTAACTGAG | TCTTCCGGGC<br>AGAAGGCCCG | GCTATCATGC<br>CGATAGTACG | CATACCGCGA<br>GTATGGCGCT |
| 3251 | AAGGTTTTGC<br>TTCCAAAACG | GCCATTCGAT<br>CGGTAAGCTA | GCTAGCCATG<br>CGATCGGTAC | TGAGCAAAAG<br>ACTCGTTTTT | GCCAGCAAAA<br>CGGTGCTTTT |
| 3301 | GGCCAGGAAC<br>CCGGTCCTTG | CGTAAAAAGG<br>GCATTTTTC  | CCGCGTTGCT<br>GGCGCAACGA | GGCGTTTTTC<br>CCGCAAAAAG | CATAGGCTCC<br>GTATCCGAGG |
| 3351 | GCCCCCCTGA<br>CGGGGGGACT | CGAGCATCAC<br>GCTCGTAGTG | AAAAATCGAC<br>TTTTTAGCTG | GCTCAAGTCA<br>CGAGTTCAGT | GAGGTGGCGA<br>CTCCACCGCT |
| 3401 | AACCCGACAG               | GACTATAAAG               | ATACCAGGCG               | TTTCCCCCTG               | GAAGCTCCCT               |

Fig. 13 (cont.)



|      |                           |                          |                          |                           |                          |
|------|---------------------------|--------------------------|--------------------------|---------------------------|--------------------------|
|      | TTGGGCTGTC                | CTGATATTTT               | TATGGTCCGC               | AAAGGGGGAC                | CTTCGAGGGA               |
| 3451 | CGTGCCTCT<br>GCACGCGAGA   | CCTGTTCCGA<br>GGACAAGGCT | CCCTGCCGCT<br>GGGACGGCGA | TACCGGATAC<br>ATGGCCTATG  | CTGTCCGCCT<br>GACAGGCGGA |
| 3501 | TTCTCCCTTC<br>AAGAGGGAAG  | GGGAAGCGTG<br>CCCTTCGCAC | GCGCTTTCTC<br>CGCGAAAGAG | ATAGCTCACG<br>TATCGAGTGC  | CTGTAGGTAT<br>GACATCCATA |
|      |                           |                          |                          | ApalI                     |                          |
|      |                           |                          |                          | ~~~~~                     |                          |
| 3551 | CTCAGTTCGG<br>GAGTCAAGCC  | TGTAGGTCGT<br>ACATCCAGCA | TCGCTCCAAG<br>AGCGAGGTTT | CTGGGCTGTG<br>GACCCGACAC  | TGCACGAACC<br>ACGTGCTTGG |
| 3601 | CCCCGTTTCA<br>GGGGCAAGTC  | CCCGACCGCT<br>GGGCTGGCGA | GCGCCTTATC<br>CGCGGAATAG | CGGTAACAT<br>GCCATTGATA   | CGTCTTGAGT<br>GCAGAACTCA |
| 3651 | CCAACCCGGT<br>GGTTGGGCCA  | AAGACACGAC<br>TTCTGTGCTG | TTATCGCCAC<br>AATAGCGGTG | TGGCAGCAGC<br>ACCGTCGTCG  | CACTGGTAAC<br>GTGACCATTG |
| 3701 | AGGATTAGCA<br>TCCTAATCGT  | GAGCGAGGTA<br>CTCGCTCCAT | TGTAGGCGGT<br>ACATCCGCCA | GCTACAGAGT<br>CGATGTCTCA  | TCTTGAAGTG<br>AGAACTTCAC |
| 3751 | GTGGCCTAAC<br>CACC GGATTG | TACGGCTACA<br>ATGCCGATGT | CTAGAAGAAC<br>GATCTTCTTG | AGTATTTGGT<br>TCATAAACCA  | ATCTGCGCTC<br>TAGACGCGAG |
| 3801 | TGCTGTAGCC<br>ACGACATCGG  | AGTTACCTTC<br>TCAATGGAAG | GGAAAAAGAG<br>CCTTTTTCTC | TTGGTAGCTC<br>AACCATCGAG  | TTGATCCGGC<br>AACTAGGCCG |
| 3851 | AAACAAACCA<br>TTTGTTTGGT  | CCGCTGGTAG<br>GGCGACCATC | CGGTGGTTTT<br>GCCACAAAAA | TTTGTTTGCA<br>AAACAAACGT  | AGCAGCAGAT<br>TCGTCGTCTA |
| 3901 | TACGCGCAGA<br>ATGCGCGTCT  | AAAAAAGGAT<br>TTTTTTCCTA | CTCAAGAAGA<br>GAGTTCTTCT | TCCTTTGATC<br>AGGAAACTAG  | TTTTCTACGG<br>AAAAGATGCC |
| 3951 | GGTCTGACGC<br>CCAGACTGCG  | TCAGTGGAAC<br>AGTCACCTTG | GAAAACTCAC<br>CTTTTGAGTG | GTTAAGGGAT<br>CAATTCCTTA  | TTTGGTCAGA<br>AAACCAGTCT |
| 4001 | TCTAGCACCA<br>AGATCGTGGT  | GGCGTTTAA<br>CCGCAAATTC  | GGCACCAATA<br>CCGTGGTTAT | ACTGCCTTAA<br>TGACGGAATT  | AAAAATTACG<br>TTTTTAATGC |
| 4051 | CCCCGCCCTG<br>GGGGCGGGAC  | CCACTCATCG<br>GGTGAGTAGC | CAGTACTGTT<br>GTCATGACAA | GTAATTCATT<br>CATTAAAGTAA | AAGCATTCTG<br>TTCGTAAGAC |
| 4101 | CCGACATGGA<br>GGCTGTACCT  | AGCCATCACA<br>TCGGTAGTGT | AACGGCATGA<br>TTGCCGTACT | TGAACCTGAA<br>ACTTGGAATT  | TCGCCAGCGG<br>AGCGGTCGCC |
| 4151 | CATCAGCACC<br>GTAGTCGTGG  | TTGTGCGCTT<br>AACAGCGGAA | GCGTATAATA<br>CGCATATTAT | TTTGCCCAT<br>AAACGGGTAT   | GTGAAAACGG<br>CACTTTTGCC |
| 4201 | GGGCGAAGAA<br>CCCGCTTCTT  | GTTGTCCATA<br>CAACAGGTAT | TTGGCTACGT<br>AACCGATGCA | TTAAATCAAA<br>AATTTAGTTT  | ACTGGTGAAA<br>TGACCACTTT |

Fig. 13 (cont.)

|      |                           |                          |                           |                          |                          |
|------|---------------------------|--------------------------|---------------------------|--------------------------|--------------------------|
| 4251 | CTCACCCAGG<br>GAGTGGGTCC  | GATTGGCTGA<br>CTAACCGACT | GACGAAAAAC<br>CTGCTTTTTTG | ATATTCTCAA<br>TATAAGAGTT | TAAACCCTTT<br>ATTTGGGAAA |
| 4301 | AGGGAAATAG<br>TCCCTTTATC  | GCCAGGTTTT<br>CGGTCCAAAA | CACCGTAACA<br>GTGGCATTGT  | CGCCACATCT<br>GCGGTGTAGA | TGCGAATATA<br>ACGCTTATAT |
| 4351 | TGTGTAGAAA<br>ACACATCTTT  | CTGCCGGAAA<br>GACGGCCTTT | TCGTCGTGGT<br>AGCAGCACCA  | ATTCACTCCA<br>TAAGTGAGGT | GAGCGATGAA<br>CTCGCTACTT |
| 4401 | AACGTTTCAG<br>TTGCAAAGTC  | TTTGCTCATG<br>AAACGAGTAC | GAAAACGGTG<br>CTTTTGCCAC  | TAACAAGGGT<br>ATTGTTCCCA | GAACACTATC<br>CTTGTGATAG |
| 4451 | CCATATCACC<br>GGTATAGTGG  | AGCTCACCGT<br>TCGAGTGGCA | CTTTCATTGC<br>GAAAGTAACG  | CATACGGAAC<br>GTATGCCTTG | TCCGGGTGAG<br>AGGCCCACTC |
| 4501 | CATTATCAG<br>GTAAGTAGTC   | GCGGGCAAGA<br>CGCCCGTTCT | ATGTGAATAA<br>TACACTTATT  | AGGCCGGATA<br>TCCGGCCTAT | AAACTTGTGC<br>TTTGAACACG |
| 4551 | TTATTTTTCT<br>AATAAAAAGA  | TTACGGTCTT<br>AATGCCAGAA | TAAAAAGGCC<br>ATTTTTCCGG  | GTAATATCCA<br>CATTATAGGT | GCTGAACGGT<br>CGACTTGCCA |
| 4601 | CTGGTTATAG<br>GACCAATATC  | GTACATTGAG<br>CATGTAAGTC | CAACTGACTG<br>GTTGACTGAC  | AAATGCCTCA<br>TTTACGGAGT | AAATGTTCTT<br>TTTACAAGAA |
| 4651 | TACGATGCCA<br>ATGCTACGGT  | TTGGGATATA<br>AACCCTATAT | TCAACGGTGG<br>AGTTGCCACC  | TATATCCAGT<br>ATATAGGTCA | GATTTTTTTC<br>CTAAAAAAG  |
| 4701 | TCCATTTTAG<br>AGGTAAAATC  | CTTCCTTAGC<br>GAAGGAATCG | TCCTGAAAAT<br>AGGACTTTTA  | CTCGATAACT<br>GAGCTATTGA | CAAAAAATAC<br>GTTTTTTATG |
| 4751 | GCCCGGTAGT<br>CGGGCCATCA  | GATCTTATTT<br>CTAGAATAAA | CATTATGGTG<br>GTAATACCAC  | AAAGTTGGAA<br>TTTCAACCTT | CCTCACCCGA<br>GGAGTGGGCT |
| 4801 | CGTCTAATGT<br>GCAGATTACA  | GAGTTAGCTC<br>CTCAATCGAG | ACTCATTAGG<br>TGAGTAATCC  | CACCCCAGGC<br>GTGGGGTCCG | TTTACACTTT<br>AAATGTGAAA |
| 4851 | ATGCTTCCGG<br>TACGAAGGCC  | CTCGTATGTT<br>GAGCATACAA | GTGTGGAATT<br>CACACCTTAA  | GTGAGCGGAT<br>CACTCGCCTA | AACAATTTCA<br>TTGTTAAAGT |
|      | M13 Reverse primer 100.0% |                          |                           | XbaI                     |                          |
|      | =====                     |                          |                           | ~~~~~                    |                          |
| 4901 | CACAGGAAAC<br>GTGTCCTTTG  | AGCTATGACC<br>TCGATACTGG | ATGATTACGA<br>TACTAATGCT  | ATTTCTAGAT<br>TAAAGATCTA | AACGAGGGCA<br>TTGCTCCCGT |
| 4951 | AAAAATGAAA<br>TTTTTACTTT  | AAGACAGCTA<br>TTCTGTCGAT | TCGCGATTGC<br>AGCGCTAACG  | AGTGGCACTG<br>TCACCGTGAC | GCTGGTTTCG<br>CGACCAAAGC |
|      | EcoRV                     |                          |                           |                          |                          |
|      | ~~~                       |                          |                           |                          |                          |
| 5001 | CTACCGTAGC<br>GATGGCATCG  | GCAGGCCGAT<br>CGTCCGGCTA |                           |                          |                          |

Fig. 13 (cont.)

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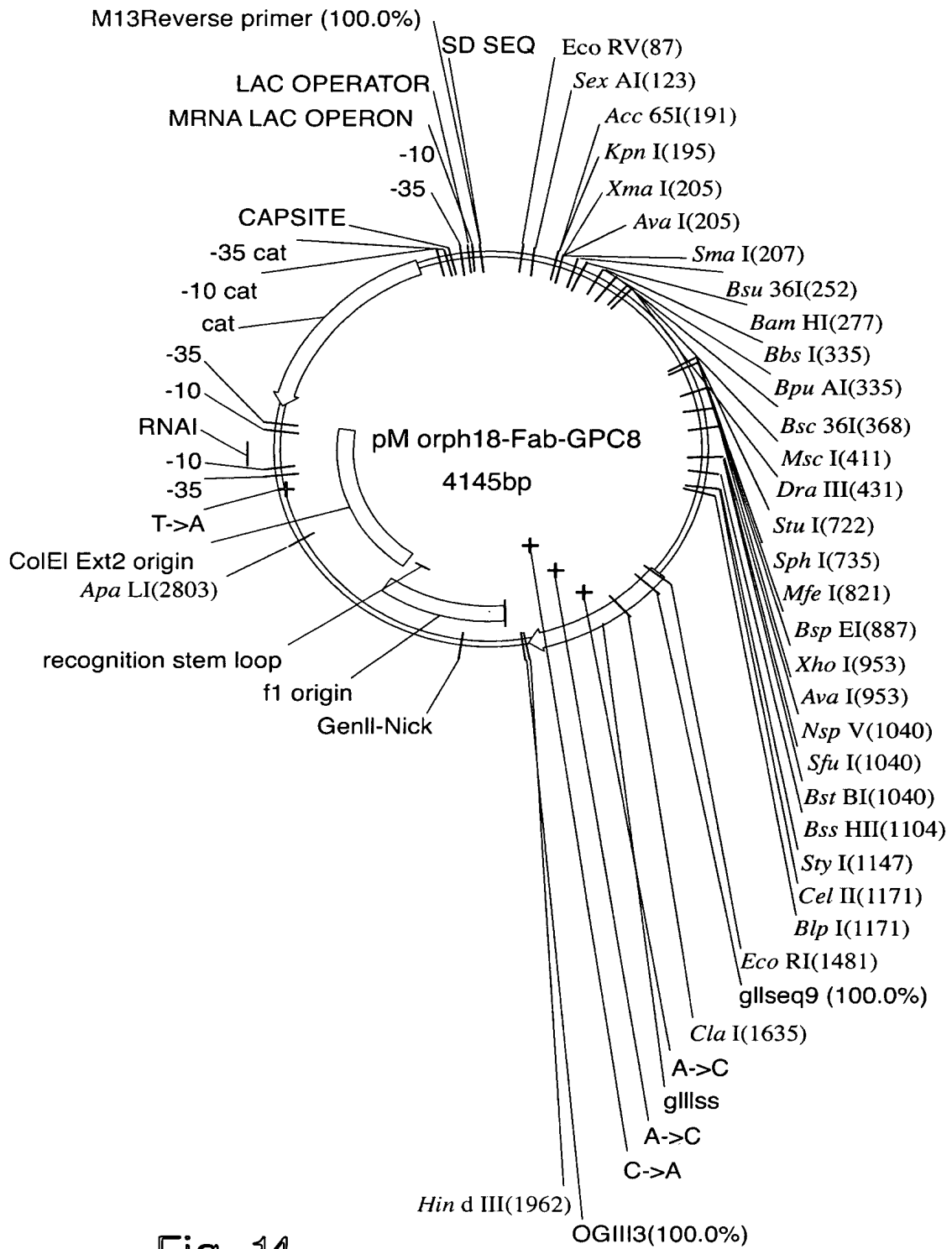


Fig. 14

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1  TCAGATAACG AGGGCAAAAA ATGAAAAAGA CAGCTATCGC GATTGCAGTG
   AGTCTATTGC TCCCGTTTTT TACTTTTTCT GTCGATAGCG CTAACGTCAC

                                     EcoRV
                                     ~~~~~~
51 GCACTGGCTG GTTTCGCTAC CGTAGCGCAG GCCGATATCG TGCTGACCCA
 CGTGACCGAC CAAAGCGATG GCATCGCGTC CGGCTATAGC ACGACTGGGT

 SexAI
                                     ~~~~~~
101 GCCGCCTTCA GTGAGTGGCG CACCAGGTCA GCGTGTGACC ATCTCGTGTA
   CGGCGGAAGT CACTCACCGC GTGGTCCAGT CGCACACTGG TAGAGCACAT

                                     KpnI
                                     ~~~~~~
 Acc65I
                                     ~~~~~~
151 GCGGCAGCAG CAGCAACATT GGCAGCAACT ATGTGAGCTG GTACCAGCAG
   CGCCGTCGTC GTCGTTGTAA CCGTCGTTGA TACACTCGAC CATGGTCGTC

      XmaI
      ~~~~~~
 SmaI
      ~~~~~~
      AvaI
      ~~~~~~
 Bsu36I
                                     ~~~~~~
201 TTGCCCCGGA CGGCGCCGAA ACTGCTGATT TATGATAACA ACCAGCGTCC
   AACGGGCCCT GCCGCGGCTT TGACGACTAA ATACTATTGT TGGTCGCAGG

      Bsu36I
      ~~~~~~
 BamHI
                                     ~~~~~~
251 CTCAGGCGTG CCGGATCGTT TTAGCGGATC CAAAAGCGGC ACCAGCGCGA
   GAGTCCGCAC GGCCTAGCAA AATCGCCTAG GTTTTCGCCG TGGTCGCGCT

                                     BpuAI
                                     ~~~~~~
 BbsI
                                     ~~~~~~
301 GCCTTGCGAT TACGGGCCTG CAAAGCGAAG ACGAAGCGGA TTATTATTGC
   CGGAACGCTA ATGCCCGGAC GTTTCGCTTC TGCTTCGCCT AATAATAACG

                                     Bsu36I
                                     ~~~~~~
351 CAGAGCTATG ACATGCCTCA GGCTGTGTTT GGCGGCGGCA CGAAGTTTAA
 GTCTCGATAC TGTACGGAGT CCGACACAAA CCGCCGCCGT GCTTCAAATT

 MscI
      ~~~~~~
                                     DraIII
                                     ~~~~~~
401 CCGTTCCTGG CCAGCCGAAA GCCGCACCGA GTGTGACGCT GTTTCGCCCG
 GGCAAGAACC GGTCGGCTTT CGGCGTGGCT CAACTGCGA CAAAGGCGGC

451 AGCAGCGAAG AATTGCAGGC GAACAAAGCG ACCCTGGTGT GCCTGATTAG
 TCGTCGCTTC TTAACGTCCG CTTGTTTCGC TGGGACCACA CGGACTAATC

501 CGACTTTTAT CCGGGAGCCG TGACAGTGGC CTGGAAGGCA GATAGCAGCC

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Fig. 14 (cont.)

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|      |            |            |             |            |             |
|------|------------|------------|-------------|------------|-------------|
|      | GCTGAAAATA | GGCCCTCGGC | ACTGTCACCG  | GACCTTCCGT | CTATCGTCGG  |
| 551  | CCGTCAAGGC | GGGAGTGGAG | ACCACCACAC  | CCTCCAAACA | AAGCAACAAC  |
|      | GGCAGTTCCG | CCCTCACCTC | TGGTGGTGTG  | GGAGGTTTGT | TTCGTTGTTG  |
| 601  | AAGTACGCGG | CCAGCAGCTA | TCTGAGCCTG  | ACGCCTGAGC | AGTGGAAGTC  |
|      | TTCATGCGCC | GGTCGTCGAT | AGACTCGGAC  | TGCGGACTCG | TCACCTTCAG  |
| 651  | CCACAGAAGC | TACAGCTGCC | AGGTCACGCA  | TGAGGGGAGC | ACCGTGGAAC  |
|      | GGTGTCTTCG | ATGTCGACGG | TCCAGTGCGT  | ACTCCCCTCG | TGGCACCTTT  |
|      |            | StuI       |             | SphI       |             |
|      |            | ~~~~~      |             | ~~~~~      |             |
| 701  | AAACCGTTGC | GCCGACTGAG | GCCTGATAAG  | CATGCGTAGG | AGAAAAATAAA |
|      | TTTGGCAACG | CGGCTGACTC | CGGACTATTC  | GTACGCATCC | TCTTTTATTT  |
| 751  | ATGAAACAAA | GCACTATTGC | ACTGGCACTC  | TTACCGTTGC | TCTTCACCCC  |
|      | TACTTTGTTT | CGTGATAACG | TGACCGTGAG  | AATGGCAACG | AGAAGTGGGG  |
|      |            | MfeI       |             |            |             |
|      |            | ~~~~~      |             |            |             |
| 801  | TGTTACCAAA | GCCCAGGTGC | AATTGAAAGA  | AAGCGGCCCG | GCCCTGGTGA  |
|      | ACAATGGTTT | CGGGTCCACG | TTAACTTTCT  | TTCGCCGGGC | CGGGACCACT  |
|      |            |            |             | BspEI      |             |
|      |            |            |             | ~~~~~      |             |
| 851  | AACCGACCCA | AACCCTGACC | CTGACCTGTA  | CCTTTTCCGG | ATTTAGCCTG  |
|      | TTGGCTGGGT | TTGGGACTGG | GACTGGACAT  | GGAAAAGGCC | TAAATCGGAC  |
| 901  | TCCACGTCTG | GCGTTGGCGT | GGGCTGGATT  | CGCCAGCCGC | CTGGGAAAGC  |
|      | AGGTGCAGAC | CGCAACCGCA | CCCAGACCTAA | GCGGTGCGCG | GACCCTTTTCG |
|      |            | XhoI       |             |            |             |
|      |            | ~~~~~      |             |            |             |
|      |            | AvaI       |             |            |             |
|      |            | ~~~~~      |             |            |             |
| 951  | CCTCGAGTGG | CTGGCTCTGA | TTGATTGGGA  | TGATGATAAG | TATTATAGCA  |
|      | GGAGCTCACC | GACCGAGACT | AACTAACCCT  | ACTACTATTC | ATAATATCGT  |
|      |            |            |             | BstBI      |             |
|      |            |            |             | ~~~~~      |             |
|      |            |            |             | SfuI       |             |
|      |            |            |             | ~~~~~      |             |
|      |            |            |             | NspV       |             |
|      |            |            |             | ~~~~~      |             |
| 1001 | CCAGCCTGAA | AACGCGTCTG | ACCATTAGCA  | AAGATACTTC | GAAAAATCAG  |
|      | GGTCGGAATT | TTGCGCAGAC | TGGTAATCGT  | TTCTATGAAG | CTTTTATGTC  |
| 1051 | GTGGTGCTGA | CTATGACCAA | CATGGACCCG  | GTGGATACGG | CCACCTATTA  |
|      | CACCACGACT | GATACTGGTT | GTACCTGGGC  | CACCTATGCC | GGTGGATAAT  |
|      |            | BssHII     |             |            | StyI        |
|      |            | ~~~~~      |             |            | ~~~~~       |
| 1101 | TTGCGCGCGT | TCTCCTCGTT | ATCGTGGTGC  | TTTGATTAT  | TGGGGCCAAG  |
|      | AACGCGCGCA | AGAGGAGCAA | TAGCACCACG  | AAAATAATA  | ACCCCGGTTT  |

BlpI

Fig. 14 (cont.)

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StyI
~
1151 GCACCCTGGT GACGGTTAGC TCAGCGTCGA CCAAAGGTCC AAGCGTGTTT
 CGTGGGACCA CTGCCAATCG AGTCGCAGCT GGTTTCCAGG TTCGCACAAA

1201 CCGCTGGCTC CGAGCAGCAA AAGCACCAGC GGCGGCACGG CTGCCCTGGG
 GGCGACCGAG GCTCGTCGTT TTCGTGGTCG CCGCCGTGCC GACGGGACCC

1251 CTGCCTGGTT AAAGATTATT TCCCGBAACC AGTCACCGTG AGCTGGAACA
 GACGGACCAA TTTCTAATAA AGGGCCTTGG TCAGTGGCAC TCGACCTTGT

1301 GCGGGGCGCT GACCAGCGGC GTGCATACCT TTCCGGCGGT GCTGCAAAGC
 CGCCCCGCGA CTGGTCGCCG CACGTATGGA AAGGCCGCCA CGACGTTTCG

1351 AGCGGCCTGT ATAGCCTGAG CAGCGTTGTG ACCGTGCCGA GCAGCAGCTT
 TCGCCGGACA TATCGGACTC GTCGCAACAC TGGCACGGCT CGTCGTGCAA

1401 AGGCACTCAG ACCTATATTT GCAACGTGAA CCATAAACCG AGCAACACCA
 TCCGTGAGTC TGGATATAAA CGTTGCACTT GGTATTGTGC TCGTTGTGGT

~
EcoRI
~
1451 AAGTGGATAA AAAAGTGGAA CCGAAAAGCG AATTCGGGGG AGGGAGCGGG
 TTCACCTATT TTTTCACCTT GGCTTTTCGC TTAAGCCCCC TCCCTCGCCC

1501 AGCGGTGATT TTGATTATGA AAAGATGGCA AACGCTAATA AGGGGGCTAT
 TCGCCACTAA AACTAATACT TTTCTACCGT TTGCGATTAT TCCCCGATA
 gIIIseq9 100.0%
 =====

1551 GACCGAAAAT GCCGATGAAA ACGCGCTACA GTCTGACGCT AAAGGCAAAC
 CTGGCTTTTA CGGCTACTTT TGC GCGATGT CAGACTGCGA TTTCCGTTTG

~
ClaI
~
1601 TTGATTCTGT CGCTACTGAT TACGGTGCTG CTATCGATGG TTTCATTGGT
 AACTAAGACA GCGATGACTA ATGCCACGAC GATAGCTACC AAAGTAACCA

1651 GACGTTTCCG GCCTTGCTAA TGGTAATGGT GCTACTGGTG ATTTTGCTGG
 CTGCAAAGGC CGGAACGATT ACCATTACCA CGATGACCAC TAAACGACC

1701 CTCTAATTCC CAAATGGCTC AAGTCGGTGA CGGTGATAAT TCACCTTTAA
 GAGATTAAGG GTTTACCGAG TTCAGCCACT GCCACTATTA AGTGGA AATT

1751 TGAATAATTT CCGTCAATAT TTACCTTCCC TCCCTCAATC GGTTGAATGT
 ACTTATTAAA GGCAGTTATA AATGGAAGGG AGGGAGTTAG CCAACTTACA

1801 CGCCCTTTTG TCTTTGGCGC TGGTAAACCA TATGAATTTT CTATTGATTG
 GCGGGAAAAC AGAAACCGCG ACCATTGTTG ATACTTAAAA GATAACTAAC

1851 TGACAAAATA AACTTATTCC GTGGTGTCTT TCGGTTTCTT TTATATGTTG
 ACTGTTTTAT TTGAATAAGG CACCACAGAA ACGCAAAGAA AATATACAAC

1901 CCACCTTTAT GTATGTATTT TCTACGTTTG CTAACATACT GCGTAATAAG
 GGTGGAAAATA CATACTAAA AGATGCAAAC GATTGTATGA CGCATTATTC

```

Fig. 14 (cont.)

## HindIII

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1951 GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
 CTCAGAACTA TTCGAACTGG ACACCTTCACT TTTTACCGCG TCTAACACGC
 OGIII3 100.0%
 =====

2001 ACATTTTTTTT TGTCTGCCGT TTAATGAAAT TGTAACGTT AATATTTTGT
 TGTAACAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

2051 TAAAATTCGC GTTAAATTTT TGTTAAATCA GCTCATTTTT TAACCAATAG
 ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC

2101 GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG
 CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

2151 GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG
 CAACTCACAA CAAGGTCAA CTTGTTCTC AGGTGATAAT TTCTTGCAAC

2201 ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA
 TGAGGTTGCA GTTTCCTCGT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

2251 CGAGAACCAT CACCCTAATC AAGTTTTTTT GGGTCGAGGT GCCGTAAAGC
 GCTCTTGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCT

2301 ACTAAATCGG AACCCCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
 TGATTTAGCC TTGGGATTTC CCTCGGGGGC TAAATCTCGA ACTGCCCCCT

2351 AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC
 TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCC

2401 GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC
 CGATCCCGCG ACCGTTTACA TCGCCAGTGC GACGCGCATT GGTGGTGTGG

2451 CGCCGCGCTT AATGCGCCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA
 GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT AACTCGTTT

2501 AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT
 TCCGGTCGTT TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA

2551 TCCATAGGCT CCGCCCCCTT GACGAGCATC AAAAAATCG ACGCTCAAGT
 AGGTATCCGA GGCGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA

2601 CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC
 GTCTCCACCG CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG

2651 TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT
 ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA

2701 ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA
 TGGACAGGCG GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT

2751 CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG
 GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC

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ApaLI

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Fig. 14 (cont.)

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|            |                           |                           |                          |                          |                           |
|------------|---------------------------|---------------------------|--------------------------|--------------------------|---------------------------|
| 2801       | TGTGCACGAA<br>ACACGTGCTT  | CCCCCGTTC<br>GGGGGGCAAG   | AGTCCGACCG<br>TCAGGCTGGC | CTGCGCCTTA<br>GACGCGGAAT | TCCGGTAACT<br>AGGCCATTGA  |
| 2851       | ATCGTCTTGA<br>TAGCAGAACT  | GTCCAACCCG<br>CAGGTTGGGC  | GTAAGACACG<br>CATTCTGTGC | ACTTATCGCC<br>TGAATAGCGG | ACTGGCAGCA<br>TGACCGTCGT  |
| 2901       | GCCACTGGTA<br>CGGTGACCAT  | ACAGGATTAG<br>TGTCCCTAATC | CAGAGCGAGG<br>GTCTCGCTCC | TATGTAGGCG<br>ATACATCCGC | GTGCTACAGA<br>CACGATGTCT  |
| 2951       | GTTCTTGAAG<br>CAAGAACTTC  | TGGTGGCCTA<br>ACCACCGGAT  | ACTACGGCTA<br>TGATGCCGAT | CACTAGAAGA<br>GTGATCTTCT | ACAGTATTTG<br>TGTCTATAAAC |
| 3001       | GTATCTGCGC<br>CATAGACGCG  | TCTGCTGTAG<br>AGACGACATC  | CCAGTTACCT<br>GGTCAATGGA | TCGGAAAAAG<br>AGCCTTTTTC | AGTTGGTAGC<br>TCAACCATCG  |
| 3051       | TCTTGATCCG<br>AGAACTAGGC  | GCAAAACAAAC<br>CGTTTGTTTG | CACCGCTGGT<br>GTGGCGACCA | AGCGGTGGTT<br>TCGCCACCAA | TTTTTGTTTG<br>AAAAACAAAC  |
| 3101       | CAAGCAGCAG<br>GTTTCGTCGTC | ATTACGCGCA<br>TAATGCGCGT  | GAAAAAAAGG<br>CTTTTTTTCC | ATCTCAAGAA<br>TAGAGTTCTT | GATCCTTTGA<br>CTAGGAAACT  |
| 3151       | TCTTTTCTAC<br>AGAAAAGATG  | GGGGTCTGAC<br>CCCCAGACTG  | GCTCAGTGGA<br>CGAGTCACCT | ACGAAAACTC<br>TGCTTTTGAG | ACGTTAAGGG<br>TGCAATTCCC  |
| 3201       | ATTTTGGTCA<br>TAAAACCAGT  | GATCTAGCAC<br>CTAGATCGTG  | CAGGCGTTTA<br>GTCCGCAAAT | AGGGCACCAA<br>TCCCGTGGTT | TAATGCCTT<br>ATTGACGGAA   |
| 3251       | AAAAAAATTA<br>TTTTTTTAAT  | CGCCCCGCCC<br>GCGGGGCGGG  | TGCCACTCAT<br>ACGGTGAGTA | CGCAGTACTG<br>GCGTCATGAC | TTGTAATTCA<br>AACATTAAGT  |
| 3301       | TTAAGCATT<br>AATTCGTAAG   | TGCCGACATG<br>ACGGCTGTAC  | GAAGCCATCA<br>CTTCGGTAGT | CAAACGGCAT<br>GTTTGCCGTA | GATGAACCTG<br>CTACTTGAC   |
| 3351       | AATCGCCAGC<br>TTAGCGGTCTG | GGCATCAGCA<br>CCGTAGTCGT  | CCTTGTCGCC<br>GGAACAGCGG | TTGCGTATAA<br>AACGCATATT | TATTTGCCCA<br>ATAAACGGGT  |
| 3401       | TAGTGAAAAC<br>ATCACTTTTG  | GGGGGCGAAG<br>CCCCCGCTTC  | AAGTTGTCCA<br>TTCAACAGGT | TATTGGCTAC<br>ATAACCGATG | GTTTAAATCA<br>CAAATTTAGT  |
| 3451       | AAACTGGTGA<br>TTTGACCACT  | AACTCACCCA<br>TTGAGTGGGT  | GGGATTGGCT<br>CCCTAACCGA | GAGACGAAAA<br>CTCTGCTTTT | ACATATTCTC<br>TGTATAAGAG  |
| 3501       | AATAAACCCCT<br>TTATTTGGGA | TTAGGGAAAT<br>AATCCCTTTA  | AGGCCAGGTT<br>TCCGGTCCAA | TTCACCGTAA<br>AAGTGGCATT | CACGCCACAT<br>GTGCGGTGTA  |
| 3551       | CTTGCGAATA<br>GAACGCTTAT  | TATGTGTAGA<br>ATACACATCT  | AACTGCCGGA<br>TTGACGGCCT | AATCGTCGTG<br>TTAGCAGCAC | GTATTCACTC<br>CATAAGTGAG  |
| +1<br>3601 | CAGAGCGATG<br>GTCTCGCTAC  | AAAACGTTTC<br>TTTTGCAAAG  | AGTTTGCTCA<br>TCAAACGAGT | TGGAAAACGG<br>ACCTTTTGCC | TGTAACAAGG<br>ACATTGTTCC  |
| 3651       | GTGAACACTA<br>CACTTGTGAT  | TCCCATATCA<br>AGGGTATAGT  | CCAGCTCACC<br>GGTCGAGTGG | GTCTTTTATT<br>CAGAAAGTAA | GCCATACGGA<br>CGGTATGCCT  |

Fig. 14 (cont.)



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3701 ACTCCGGGTG AGCATTTCATC AGGCGGGCAA GAATGTGAAT AAAGGCCGGA
 TGAGGCCAC TCGTAAGTAG TCCGCCCCTT CTTACACTTA TTTCCGGCCT

3751 TAAAACTTGT GCTTATTTTT CTTTACGGTC TTTAAAAGG CCGTAATATC
 ATTTTGAACA CGAATAAAAA GAAATGCCAG AAATTTTTC CCGCATTATAG

3801 CAGCTGAACG GTCTGGTTAT AGGTACATTG AGCAACTGAC TGAAATGCCT
 GTCGACTTGC CAGACCAATA TCCATGTAAC TCGTTGACTG ACTTTACGGA

3851 CAAAATGTTC TTTACGATGC CATTGGGATA TATCAACGGT GGTATATCCA
 GTTTTACAAG AAATGCTACG GTAACCCTAT ATAGTTGCCA CCATATAGGT

3901 GTGATTTTTT TCTCCATTTT AGCTTCCTTA GCTCCTGAAA ATCTCGATAA
 CACTAAAAAA AGAGGTAAAA TCGAAGGAAT CGAGGACTTT TAGAGCTATT

3951 CTCAAAAAAT ACGCCCGGTA GTGATCTTAT TTCATTATGG TGAAAGTTGG
 GAGTTTTTTA TCGGGGCCAT CACTAGAATA AAGTAATACC ACTTTCAACC

4001 AACCTCACCC GACGTCTAAT GTGAGTTAGC TCACTCATTG GGCACCCAG
 TTGGAGTGGG CTGCAGATTA CACTCAATCG AGTGAGTAAT CCGTGGGGTC

4051 GCTTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG
 CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC

 M13 Reverse primer 100.0%
 =====
4101 ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATT
 TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTAA

```

Fig. 14 (cont.)

MS-GPC-1:

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR  
QYGHRGGFDHWGQGTLVTVSS (SEQ ID NO: 37)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSGSKSGTSASLAITGLQSEDEADYYCQSYDFNESVF  
GGGTKLTVLG (SEQ ID NO: 38)

MS-GPC-6

VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWV  
SAISGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR  
GYGRYSPDLWGQGTLVTVSS (SEQ ID NO: 39)

VL

DIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIY  
GASSRATGVPARFSGSGSGTDFTLTISSELPEDFAVYYCQQYSNLPFTFG  
QGTEKVEIKRT (SEQ ID NO: 40)

MS-GPC-8

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

Fig. 15

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMPQAV  
FGGGTKLTVLG (SEQ ID NO: 42)

MS-GPC-10

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
QLHYRGGFDLWGQGTLVTVSS (SEQ ID NO: 43)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLTMGVF  
GGGTKLTVLG (SEQ ID NO: 44)

MS-GPC-8-6

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF  
GGGTKLTVLG (SEQ ID NO: 46)

MS-GPC-8-10

VH

Fig. 15 (cont.)

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLIRHVF  
GGGTKLTVLG (SEQ ID NO: 48)

MS-GPC-8-17

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSIVYVF  
GGGTKLTVLG (SEQ ID NO: 50)

MS-GPC-8-27

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

Fig. 15 (cont.)

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV  
FGGGTKLTVLG (SEQ ID NO: 52)

MS-GPC-8-6-13

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGANYVTWYQQLPGTAPKLLIYD  
NNQRPSGVPDRFSGSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVFG  
GGTKLTVLG (SEQ ID NO: 54)

MS-GPC-8-10-57

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVQWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSGSKSGTSASLAITGLQSEDEADYYCQSYDLIRHVF  
GGGTKLTVLG (SEQ ID NO: 56)

MS-GPC-8-27-41

VH

Fig. 15 (cont.)

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVQWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV  
FGGGTKLTVLG (SEQ ID NO: 58)

MS-GPC-8-1

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSHYVF  
GGGTKLTVLG (SEQ ID NO: 28)

MS-GPC-8-9

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDIQLHVF  
GGGTKLTVLG (SEQ ID NO: 31)

Fig. 15 (cont.)

MS-GPC-8-18

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSIVF  
GGGTKLTVLG (SEQ ID NO: 32)

MS-GPC-8-6-2

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGSNYVHWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF  
GGGTKLTVLG (SEQ ID NO: 45)

MS-GPC-8-6-19

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

Fig. 15 (cont.)

VL

DIVLTQPPSVSGAPGQRTVISCSESNIGSNYVAWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF  
GGGTKLTVLG (SEQ ID NO: 47)

MS-GPC-8-6-27

VH

QVQLKESGPALVKPTQTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTVISCSDSNIGANYVTWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF  
GGGTKLTVLG (SEQ ID NO: 49)

MS-GPC-8-6-45

VH

QVQLKESGPALVKPTQTLTLCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRTVISCSEPNIGSNYVFWYQQLPGTAPKLLIYD  
NNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVFG  
GGTKLTVLG (SEQ ID NO: 51)

MS-GPC-8-6-47

Fig. 15 (cont.)



VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGSNYVSWYQQLPGTSPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVF  
GGGTKLTVLG (SEQ ID NO: 53)

MS-GPC-8-27-7

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVGWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV  
FGGGTKLTVLG (SEQ ID NO: 55)

MS-GPC-8-27-10

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEW  
LALIDWDDDKYYSTSLKTRLTISKDTSKNQVVLTMNMDPVDTATYYCAR  
SPRYRGAFDYWGQGTLVTVSS (SEQ ID NO: 41)

VL

Fig. 15 (cont.)

DIVLTQPPSVSGAPGQRVTISCSGSESNIGANYVNWYQQLPGTAPKLLIY  
DNNQRPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHV  
FGGGTKLTVLG (SEQ ID NO: 57)

Fig. 15 (cont.)

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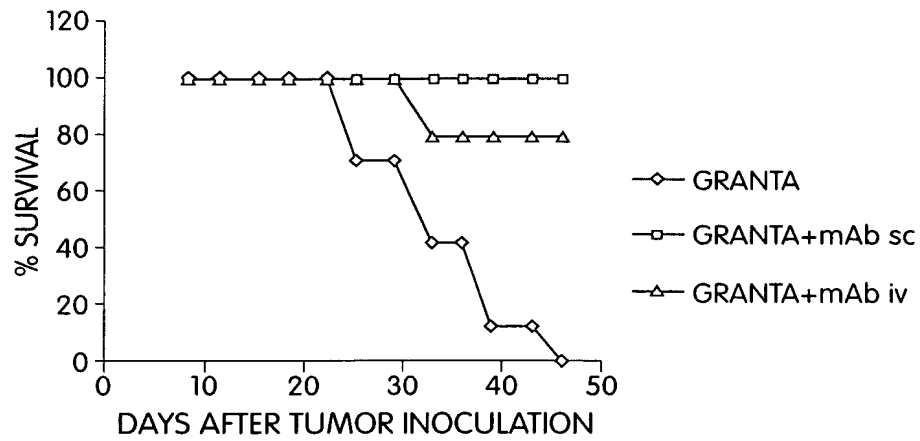


Fig. 16A

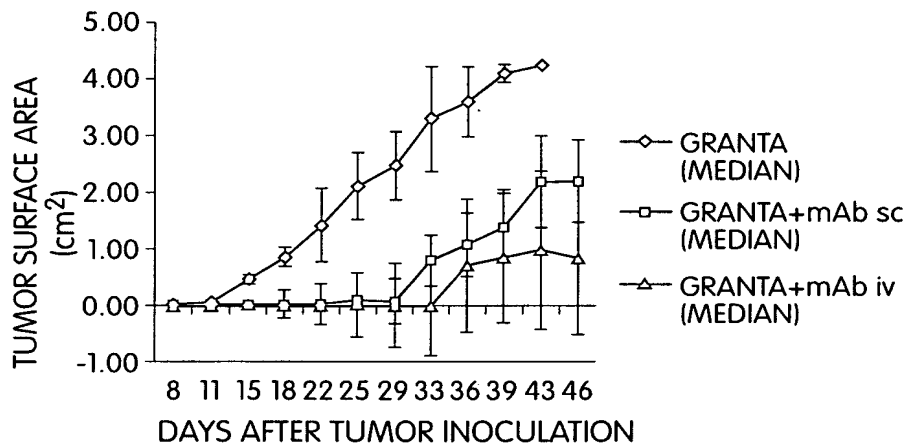


Fig. 16B

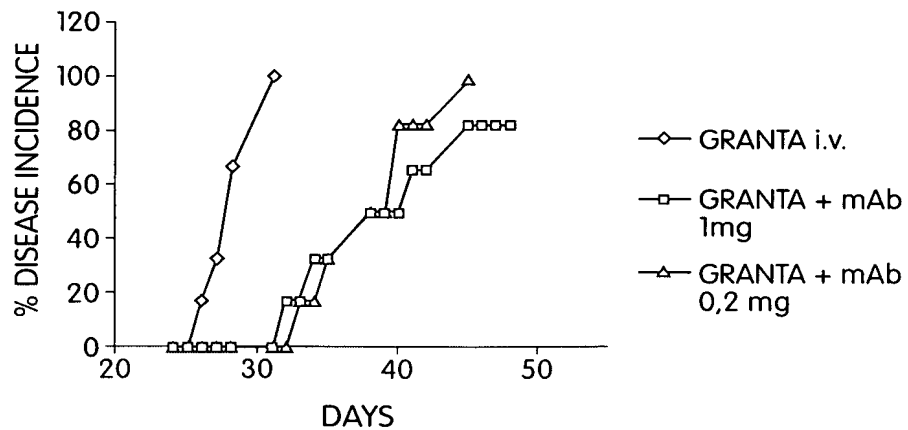
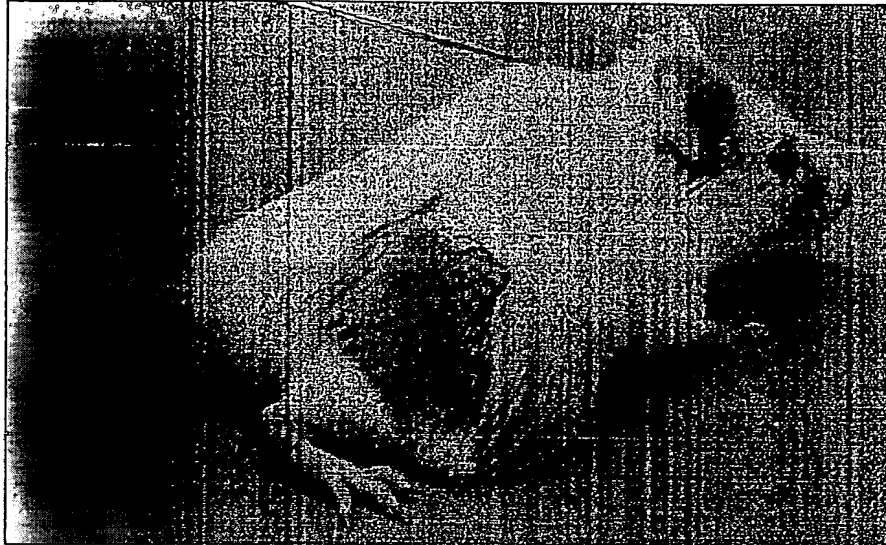


Fig. 16C



MOUSE #2, UNTREATED, DAY 32; TUMOR AREA 4.76 cm<sup>2</sup>

Fig. 16D



MOUSE #13, mAb i.v., DAY 32; TUMOR AREA 0.01 cm<sup>2</sup>

Fig. 16E